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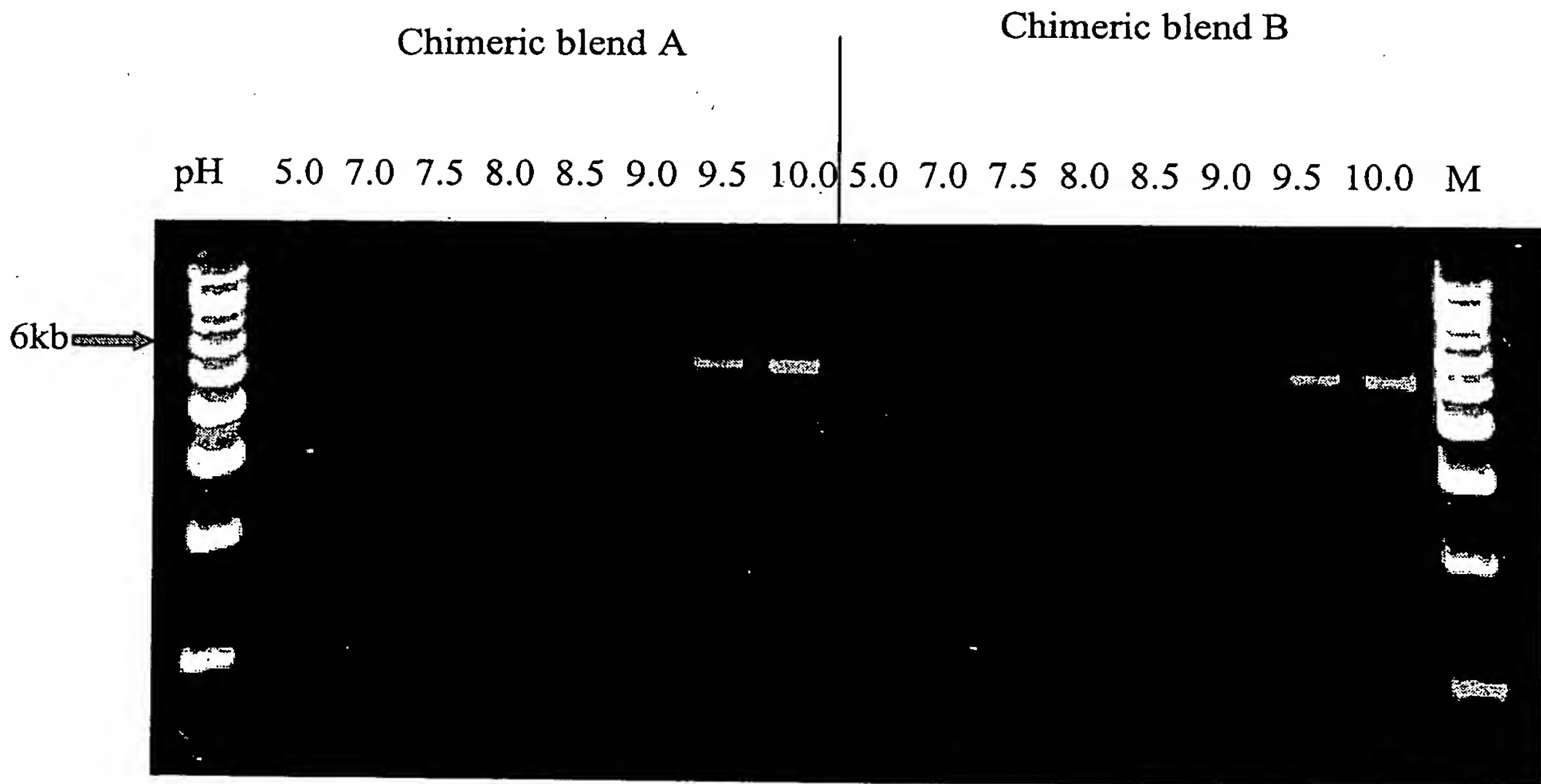
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Fig. 1



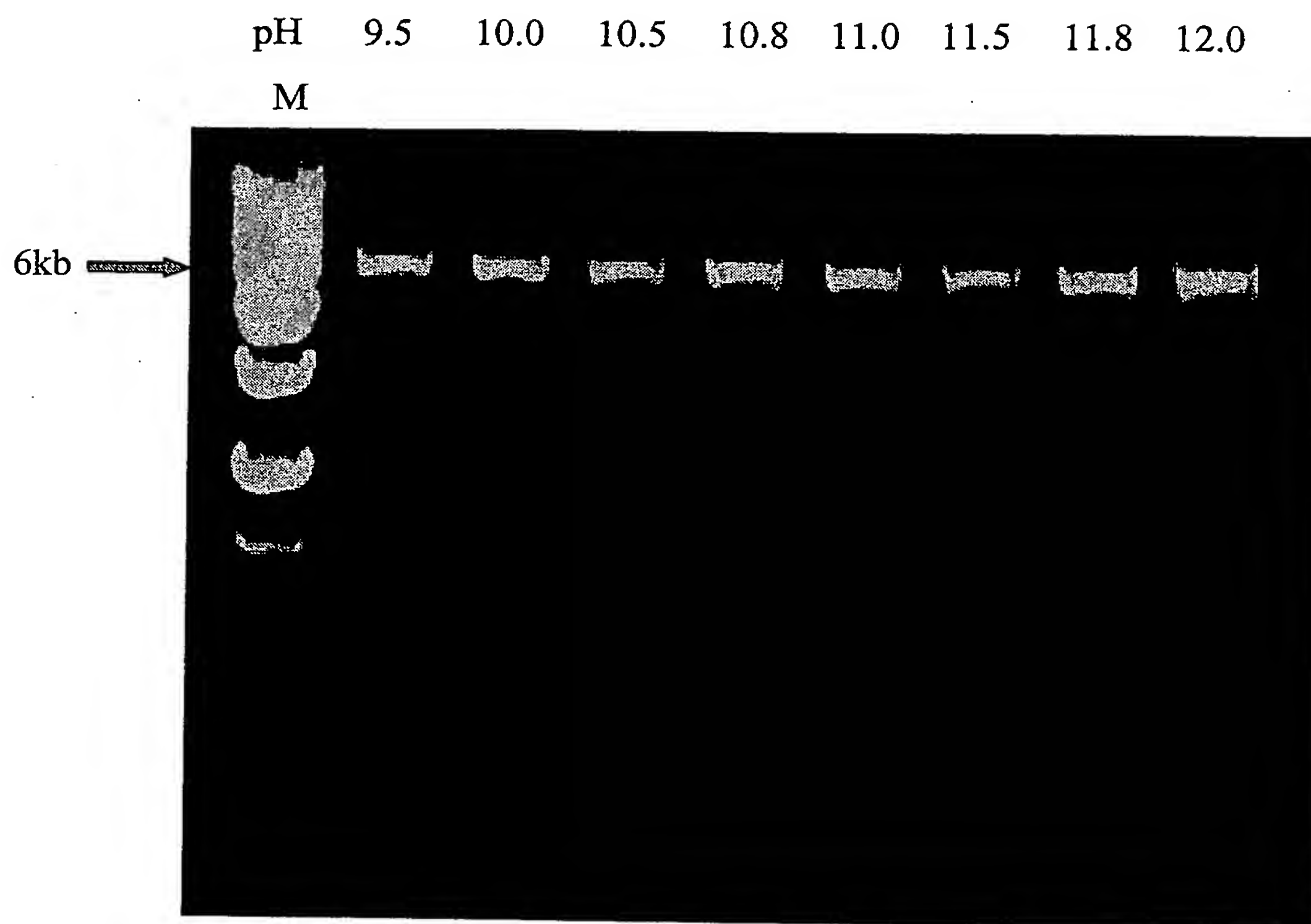
1/186

Fig. 2

6kb BG

15"/kb - 1'-30"

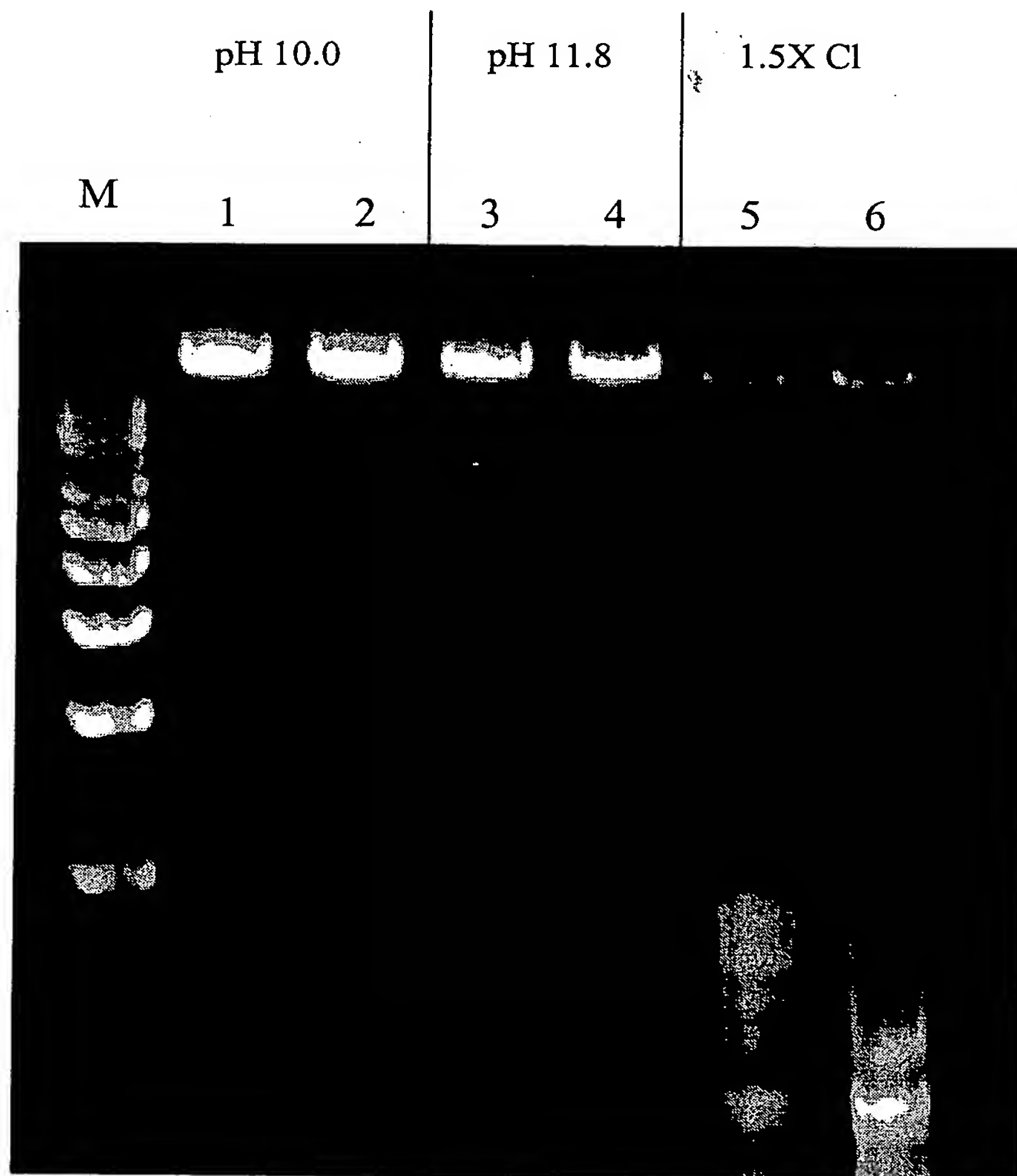
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2/186

Fig. 3

19kb BG
30''/kb - 9.5' extension

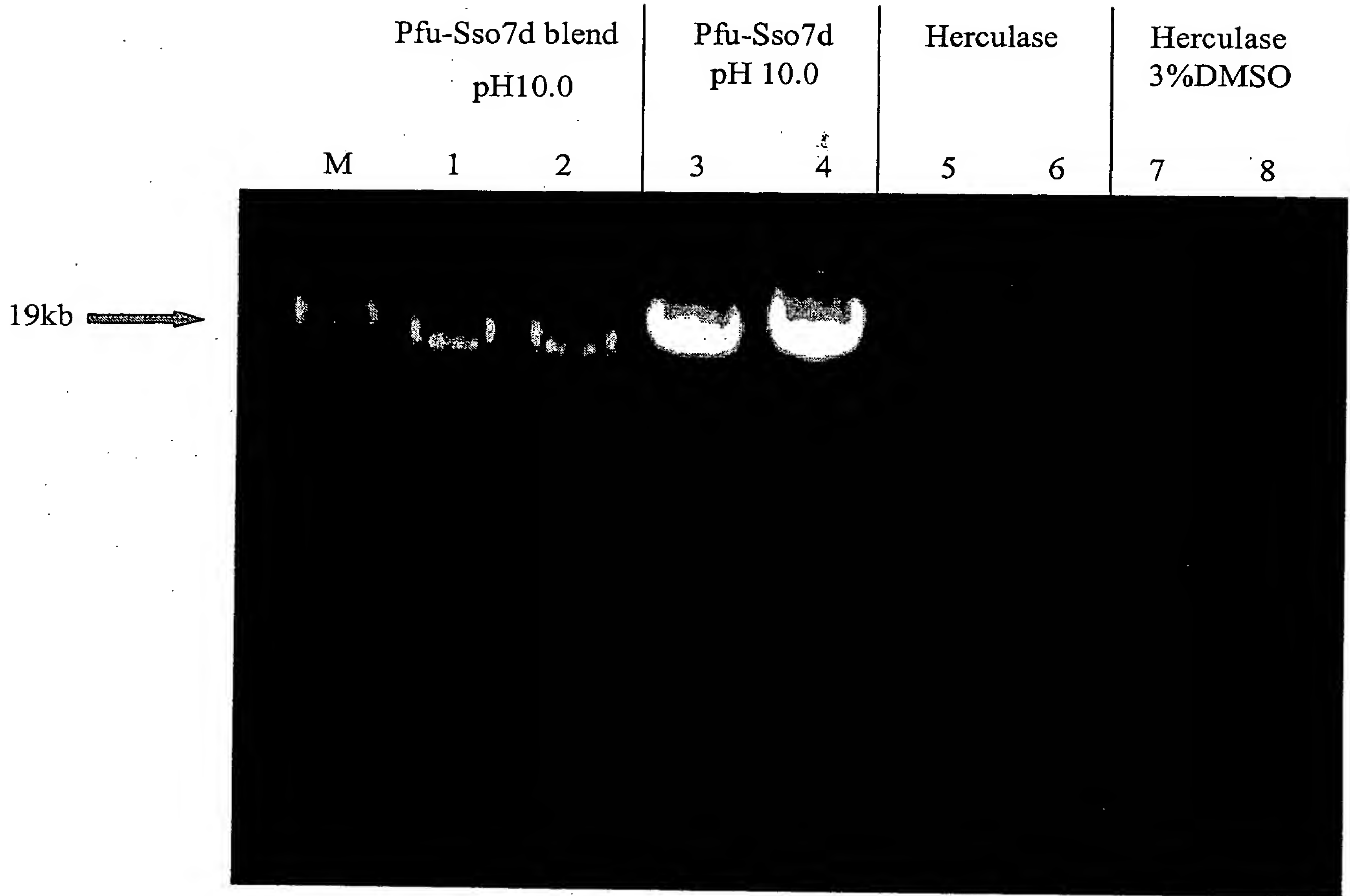


3/186

Fig. 4

19kb BG

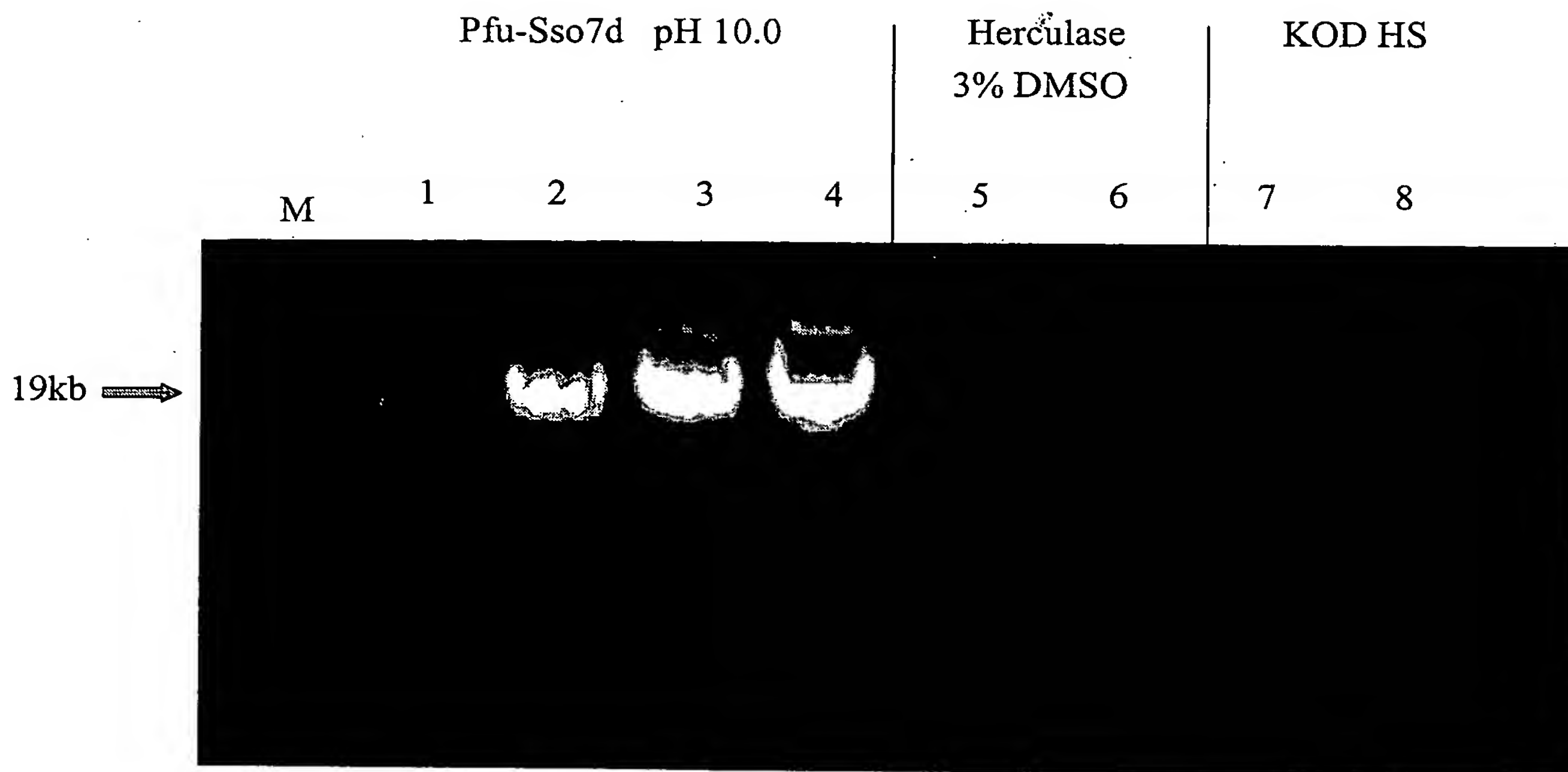
30"/kb - 9.5' extension



4/180

Fig. 5

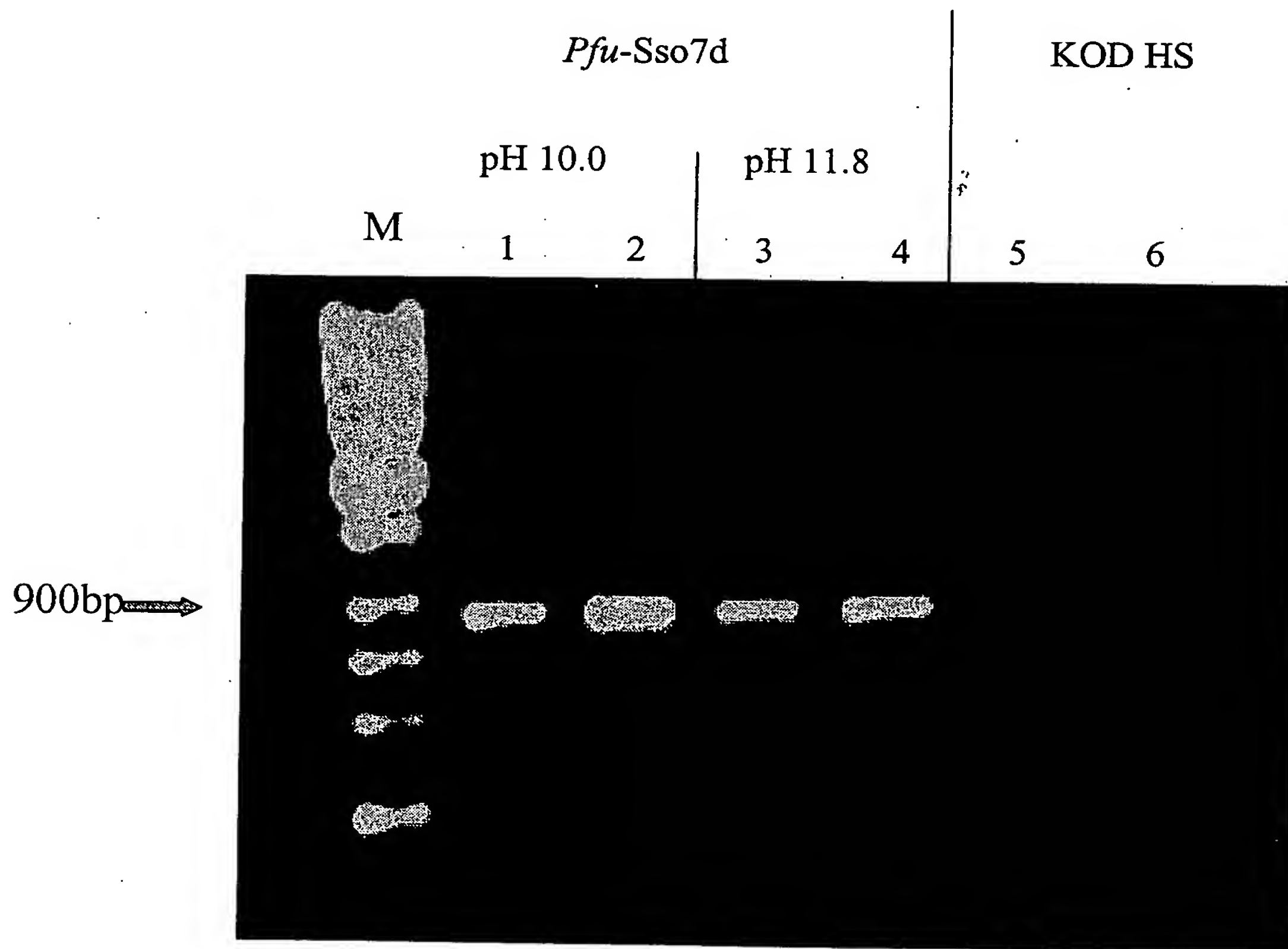
19kb BG
30"/kb - 9.5' extension



5/186

Fig. 6

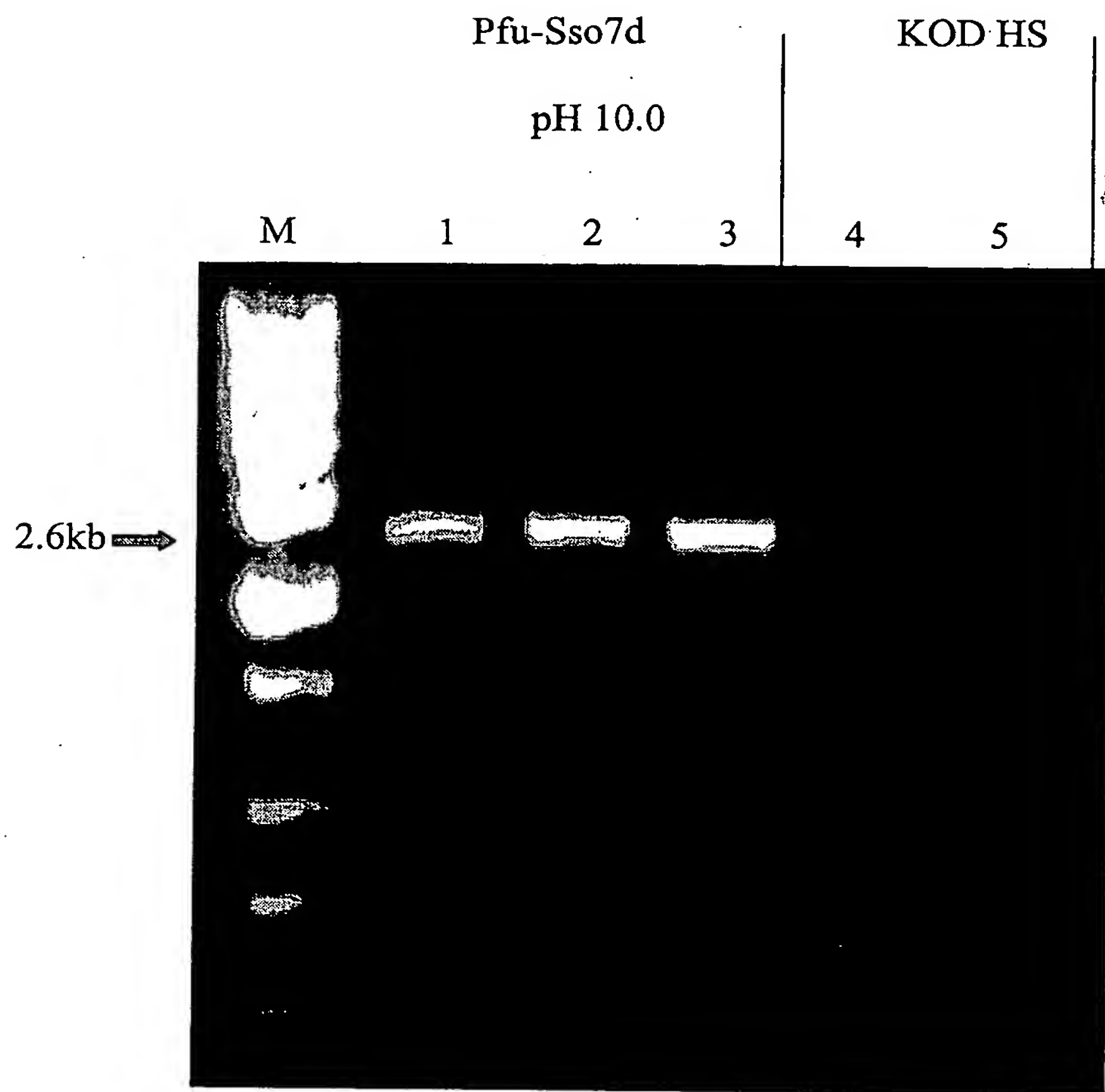
900bp H α AT
1''/kb - 1'' extension



6/186

Fig. 7

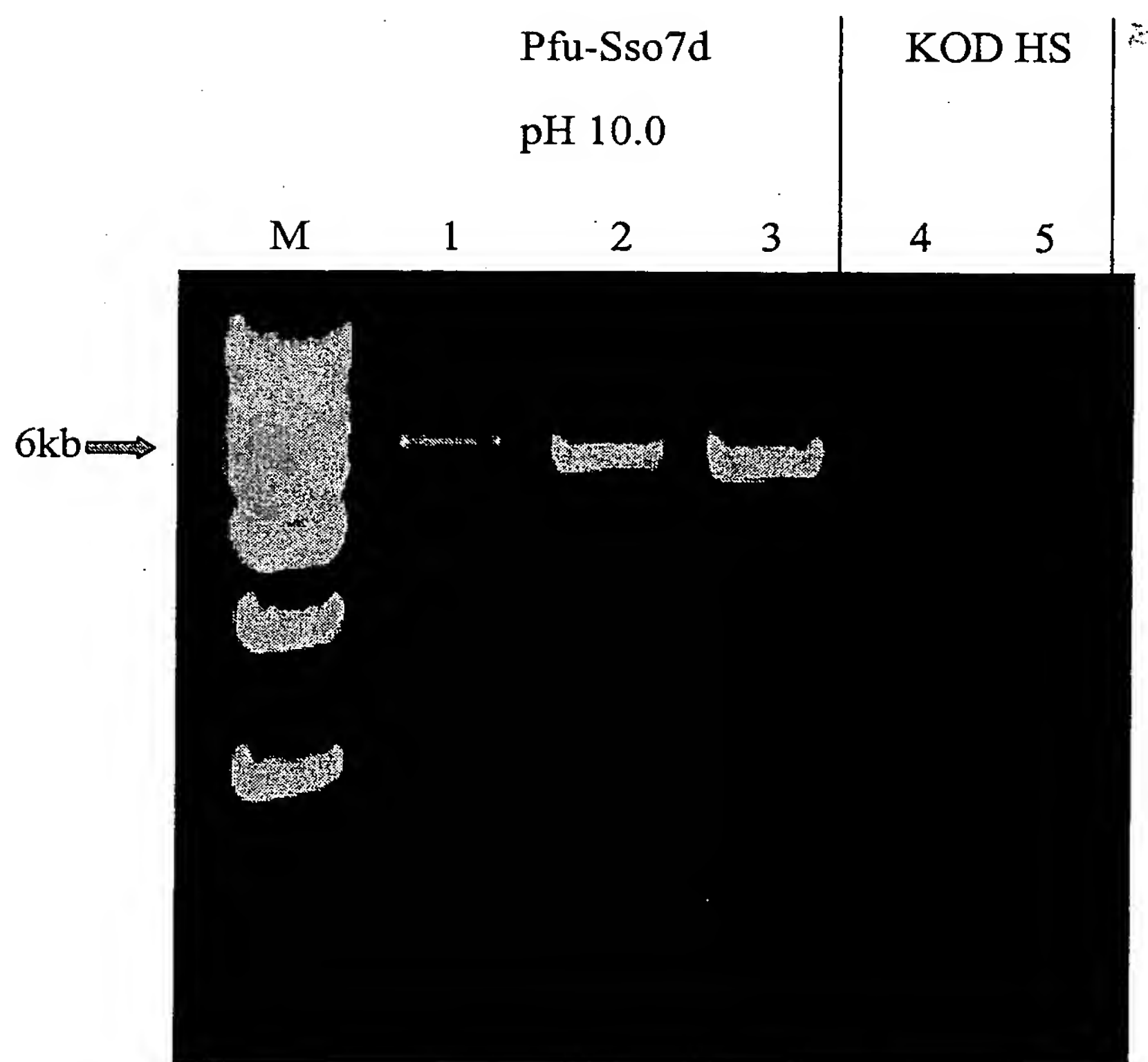
2.6kb H α AT
2''/kb - 5'' extension



7/186

Fig. 8

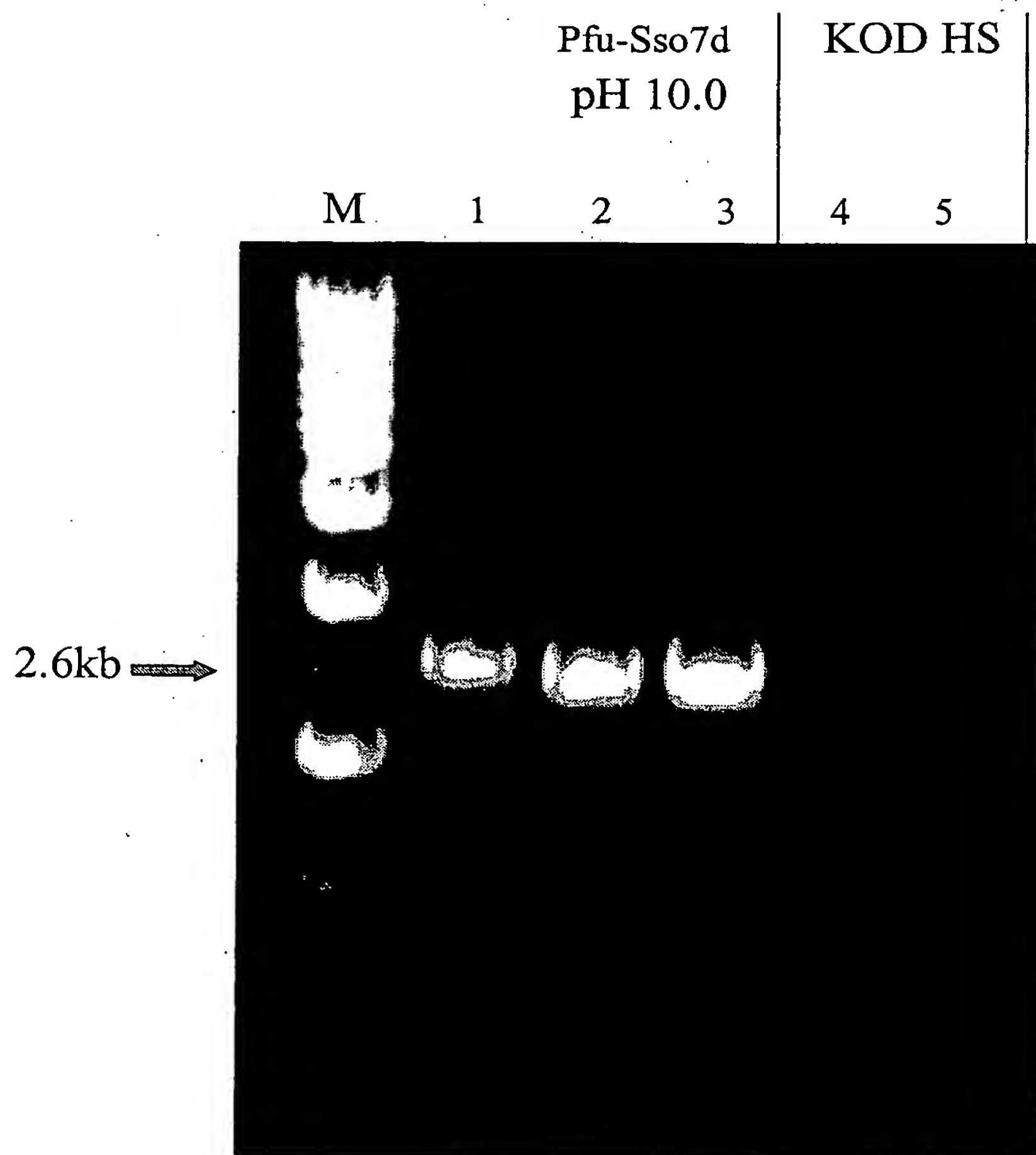
6kb BG
10"/kb - 1' extension



8/186

Fig. 9

2.6kb H α AT
30"/kb - 1'. 18" extension



9/186

Figure 10. Oligonucleotide Primers for QuikChange Mutagenesis

V93E#1

5'-gAACATCCCCAAGATgAACCCACTATTAgAgAAAAA-3' (SEQ ID NO: 6)

V93E#2

5'-CTTTTCTCTAATAgTgggTTCATCTTggggATgTTC-3' (SEQ ID NO: 7)

V93R#1

5'-gAACATCCCCAAGATgAACCCACTATTAgAgAAAAA-3' (SEQ ID NO: 8)

V93R#2

5'-CTTTTCTCTAATAgTgggTCTATCTTggggATgTTC-3' (SEQ ID NO: 9)

V93N#1

5'-gAACATCCCCAAGATgAACCCCACTATTAgAgAAAAA-3' (SEQ ID NO: 10)

V93N#2

5'-CTTTTCTCTAATAgTggggTTATCTTggggATgTTC-3' (SEQ ID NO: 11)

V93H#1

5'-gAACATCCCCAAGATgAACCCCACTATTAgAgAAAAA-3' (SEQ ID NO: 12)

V93H#2

5'-CTTTTCTCTAATAgTggggTgATCTTggggATgTTC-3' (SEQ ID NO: 13)

V93X (for saturation mutagenesis; obtained V93G and V93L mutants from library)

5'-(Phosphate)gAACATCCCCAAGATgNNKCCCACTATTAgAgAAAAA-3' (SEQ ID NO: 14)

V93K#1

Fig. 10 (cont)

5'-gAACATCCCCAAGATAAACCCACTATTAgAg-3' (SEQ ID NO: 15)

V93K#2

5'-CTCTAATAgTgggTTTATCTTggggATgTTC-3' (SEQ ID NO: 16)

QCM#1 5'-(Phosphate)gAACATCCCCAAGATgCACCACTATTAgAgAAAAAg-(SEQ ID NO: 17)

Alanine

QCM#2 5'-(Phosphate)gAACATCCCCAAGATgACCACTATTAgAgAAAAAg-3'(SEQ ID NO: 18)

Aspartic Acid

QCM#3 5'-(Phosphate)gAACATCCCCAAGATTgCCCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 19)

Cysteine

QCM#4 5'-(Phosphate)gAACATCCCCAAGATATACCACTATTAgAgAAAAAg-3' (SEQ ID NO: 20)

Isoleucine

QCM#5 5'-(Phosphate)gAACATCCCCAAGATATgCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 21)

Methionine

QCM#6 5'-(Phosphate)gAACATCCCCAAGATTTCCCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 22)

Phenylalanine

11/186

Fig. 10 (cont)

QCM#7 5'-(Phosphate)gAACATCCCCAAgATCCTCCCCTACTATTAgAgAAAAAg-3' (SEQ ID NO: 23)

Proline

QCM#8 5'-(Phosphate)gAACATCCCCAAgATAgCCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 23)

Serine

QCM#9 5'-(Phosphate)gAACATCCCCAAgATACCCCCTACTATTAgAgAAAAAg-3' (SEQ ID NO: 24)

Threonine

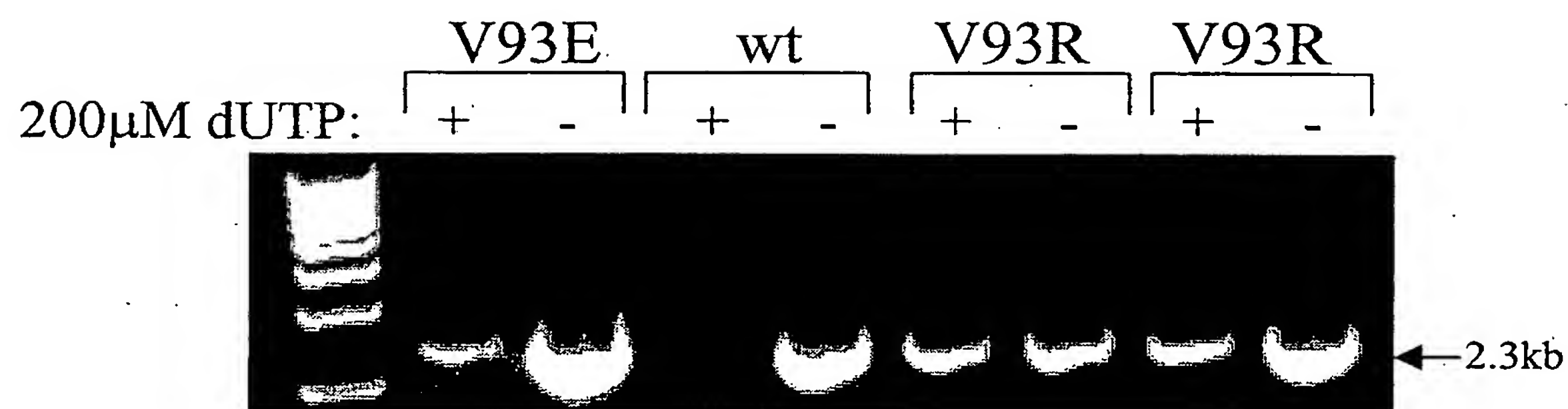
QCM#10 5'-(Phosphate)gAACATCCCCAAgATTACCCCCTACTATTAgAgAAAAAg-3' (SEQ ID NO: 25)

Tyrosine

QCM#11 5'-(Phosphate)gAACATCCCCAAgATTggCCCCTACTATTAgAgAAAAAg-3' (SEQ ID NO: 26)

Tryptophan

a.)



b.)

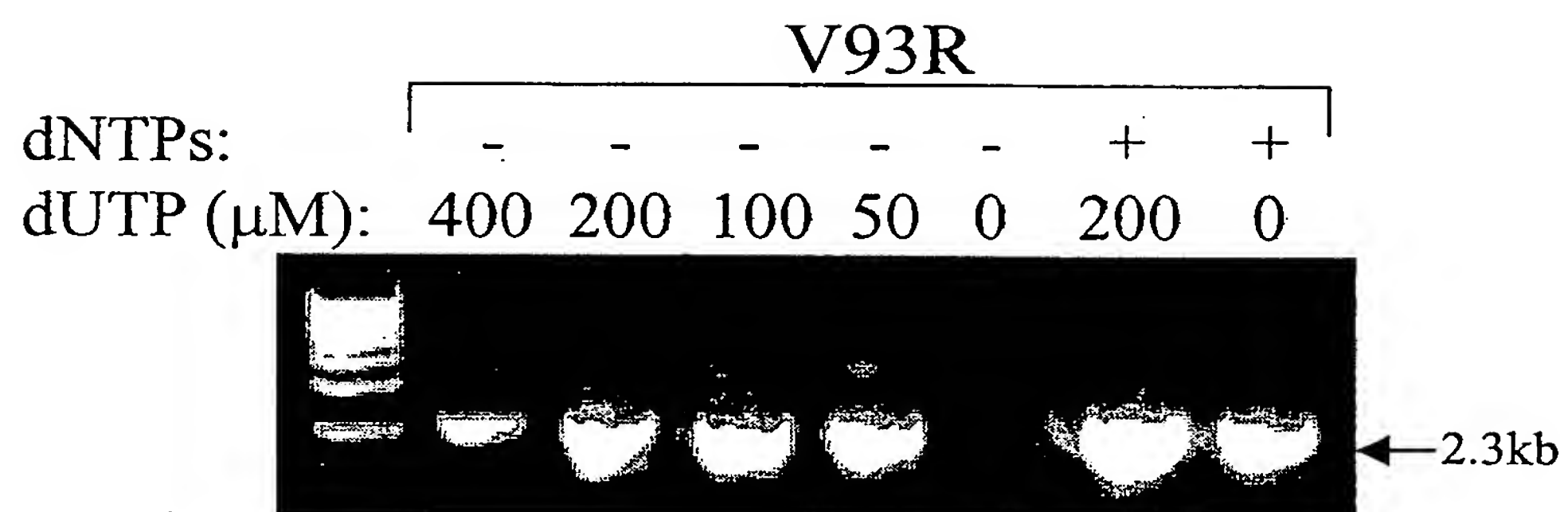


Figure 11

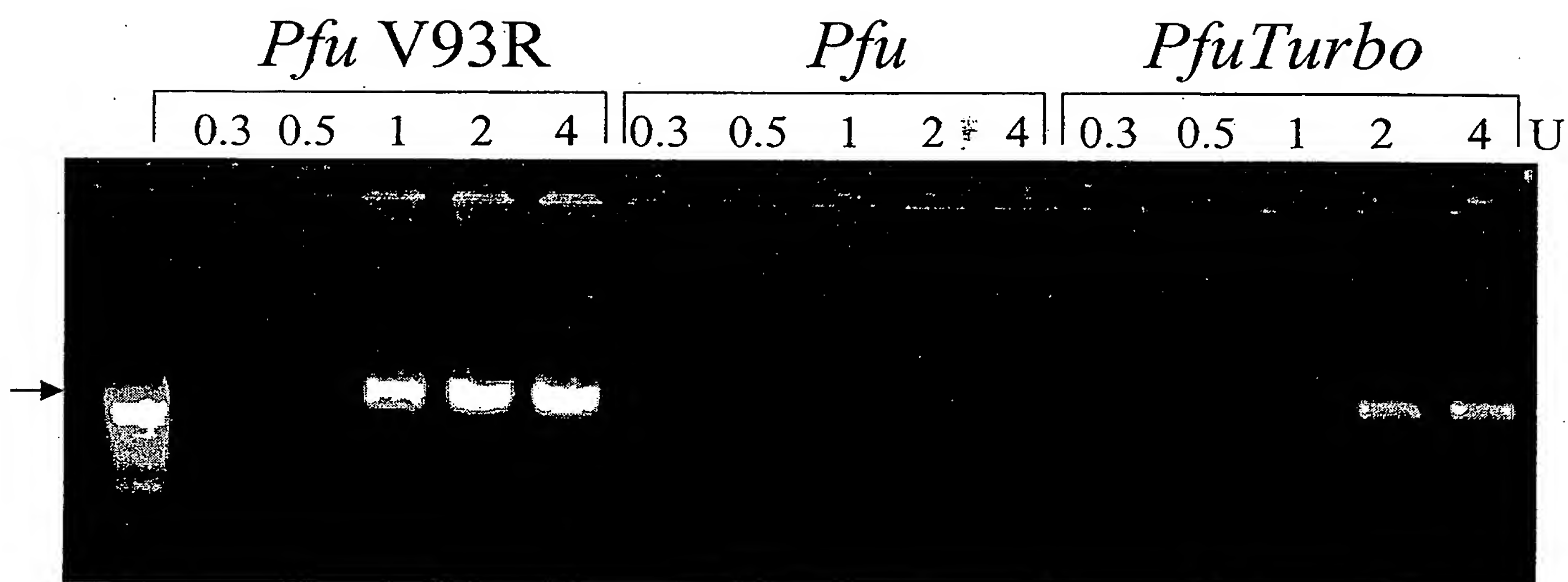


Figure 12

14/186

FIGURE 13A

PFU DNA POLYMERASE

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG	ATGTGGATTA	CATAACTGAA	GAAGGAAAAC	CTGTTATTAG	GCTATTCAAA	60
AAAGAGAACG	GAAAATTTAA	GATAGAGCAT	GATAGAACTT	TTAGACCATA	CATTTACGCT	120
CTTCTCAGGG	ATGATTCAAA	GATTGAAGAA	GTTAAGAAAA	TAACGGGGGA	AAGGCATGGA	180
AAGATTGTGA	GAATTGTTGA	TGTAGAGAAG	GTTGAGAAAA	AGTTTCTCGG	CAAGCCTATT	240
ACCGTGTGGA	AACTTTATTT	GGAACATCCC	CAAGATXXXC	CCACTATTAG	AGAAAAAGTT	300
AGAGAACATC	CAGCAGTTGT	GGACATCTTC	GAATACGATA	TTCCATTTGC	AAAGAGATAC	360
CTCATCGACA	AAGGCCTAAT	ACCAATGGAG	GGGGAAGAAG	AGCTAAAGAT	TCTTGCCTTC	420
GATATAGAAA	CCCTCTATCA	CGAAGGAGAA	GAGTTTGGAA	AAGGCCCAAT	TATAATGATT	480
AGTTATGCAG	ATGAAAATGA	AGCAAAGGTG	ATTACTTGGA	AAAACATAGA	TCTTCCATAC	540
GTTGAGGTTG	TATCAAGCGA	GAGAGAGATG	ATAAAGAGAT	TTCTCAGGAT	TATCAGGGAG	600
AAGGATCCTG	ACATTATAGT	TACTTATAAT	GGAGACTCAT	TCGCATTCCC	ATATTTAGCG	660
AAAAGGGCAG	AAAAACTTGG	GATTAAATTA	ACCATTGGAA	GAGATGGAAG	CGAGCCCAAG	720
ATGCAGAGAA	TAGGCGATAT	GACGGCTGTA	GAAGTCAAGG	GAAGAATACA	TTTCGACTTG	780
TATCATGTAA	TAACAAGGAC	AATAAATCTC	CCAACATACA	CACTAGAGGC	TGTATATGAA	840
GCAATTTTGT	GAAAGCCAAA	GGAGAAGGTA	TACGCCGACG	AGATAGCAAA	AGCCTGGGAA	900
AGTGGAGAGA	ACCTTGAGAG	AGTTGCCAAA	TACTCGATGG	AAGATGCAAA	GGCAACTTAT	960
GAACTCGGGA	AAGAATTCCT	TCCAATGGAA	ATTCAGCTTT	CAAGATTAGT	TGGACAACCT	1020
TTATGGGATG	TTTCAAGGTC	AAGCACAGGG	AACCTTGTAG	AGTGGTTCTT	ACTTAGGAAA	1080
GCCTACGAAA	GAAACGAAGT	AGCTCCAAAC	AAGCCAAGTG	AAGAGGAGTA	TCAAAGAAGG	1140
CTCAGGGAGA	GCTACACAGG	TGGATTCGTT	AAAGAGCCAG	AAAAGGGGTT	GTGGGAAAAC	1200
ATAGTATACC	TAGATTTTAG	AGCCCTATAT	CCCTCGATTA	TAATTACCCA	CAATGTTTCT	1260
CCCGATACTC	TAAATCTTGA	GGGATGCAAG	AACTATGATA	TCGCTCCTCA	AGTAGGCCAC	1320
AAGTTCTGCA	AGGACATCCC	TGGTTTTATA	CCAAGTCTCT	TGGGACATTT	GTTAGAGGAA	1380
AGACAAAAGA	TTAAGACAAA	AATGAAGGAA	ACTCAAGATC	CTATAGAAAA	AATACTCCTT	1440
GACTATAGAC	AAAAGCGAT	AAAACCTCTA	GCAAATTCTT	TCTACGGATA	TTATGGCTAT	1500
GCAAAAGCAA	GATGGTACTG	TAAGGAGTGT	GCTGAGAGCG	TTACTGCCTG	GGGAAGAAAG	1560
TACATCGAGT	TAGTATGGAA	GGAGCTCGAA	GAAAAGTTTG	GATTTAAAGT	CCTCTACATT	1620
GACACTGATG	GTCTCTATGC	AACTATCCCA	GGAGGAGAAA	GTGAGGAAAT	AAAGAAAAAG	1680
GCTCTAGAAT	TTGTAAAATA	CATAAATTCA	AAGCTCCCTG	GACTGCTAGA	GCTTGAATAT	1740
GAAGGGTTTT	ATAAGAGGGG	ATTCTTCGTT	ACGAAGAAGA	GGTATGCAGT	AATAGATGAA	1800
GAAGGAAAAG	TCATTACTCG	TGGTTTAGAG	ATAGTTAGGA	GAGATTGGAG	TGAAATTGCA	1860
AAAGAACTC	AAGCTAGAGT	TTTGAGAGACA	ATACTAAAAC	ACGGAGATGT	TGAAGAAGCT	1920
GTGAGAATAG	TAAAAGAAGT	AATACAAAAG	CTTGCCAATT	ATGAAATTCC	ACCAGAGAAG	1980
CTCGCAATAT	ATGAGCAGAT	AACAAGACCA	TTACATGAGT	ATAAGGCGAT	AGGTCCTCAC	2040
GTAGCTGTTG	CAAAGAAACT	AGCTGCTAAA	GGAGTTAAAA	TAAAGCCAGG	AATGGTAATT	2100
GGATACATAG	TACTTAGAGG	CGATGGTCCA	ATTAGCAATA	GGGCAATTCT	AGCTGAGGAA	2160
TACGATCCCA	AAAAGCACAA	GTATGACGCA	GAATATTACA	TGGAGAACCA	GGTTCTTCCA	2220
GCGGTACTTA	GGATATTGGA	GGGATTTGGA	TACAGAAAGG	AAGACCTCAG	ATACCAAAG	2280
ACAAGACAAG	TCGGCCTAAC	TTCCTGGCTT	AACATTAAAA	AATCCTAG		2328

PFU DNA POLYMERASE

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG	ATGTGGATTA	CATAACTGAA	GAAGGAAAAC	CTGTTATTAG	GCTATTCAAA	60
AAAGAGAACG	GAAAATTTAA	GATAGAGCAT	GATAGAACTT	TTAGACCATA	CATTTACGCT	120
CTTCTCAGGG	ATGATTCAAA	GATTGAAGAA	GTTAAGAAAA	TAACGGGGGA	AAGGCATGGA	180
AAGATTGTGA	GAATTGTTGA	TGTAGAGAAG	GTTGAGAAAA	AGTTTCTCGG	CAAGCCTATT	240
ACCGTGTGGA	AACTTTATTT	GGAACATCCC	CAAGATXXXC	CCACTATTAG	AGAAAAAGTT	300

Fig. 13A (cont)

AGAGAACATC	CAGCAGTTGT	GGACATCTTC	GAATACGATA	TTCCATTTGC	AAAGAGATAC	360
CTCATCGACA	AAGGCCTAAT	ACCAATGGAG	GGGGAAGAAG	AGCTAAAGAT	TCTTGCCTTC	420
GATATAGAAA	CCCTCTATCA	CGAAGGAGAA	GAGTTTGGAA	AAGGCCCAAT	TATAATGATT	480
AGTTATGCAG	ATGAAAATGA	AGCAAAGGTG	ATTACTTGGA	AAAACATAGA	TCTTCCATAC	540
GTTGAGGTTG	TATCAAGCGA	GAGAGAGATG	ATAAAGAGAT	TTCTCAGGAT	TATCAGGGAG	600
AAGGATCCTG	ACATTATAGT	TACTTATAAT	GGAGACTCAT	TCGCATTCCC	ATATTTAGCG	660
AAAAGGGCAG	AAAAACTTGG	GATTAAATTA	ACCATTGGAA	GAGATGGAAG	CGAGCCCAAG	720
ATGCAGAGAA	TAGGCGATAT	GACGGCTGTA	GAAGTCAAGG	GAAGAATACA	TTTCGACTTG	780
TATCATGTAA	TAACAAGGAC	AATAAATCTC	CCAACATACA	CACTAGAGGC	TGTATATGAA	840
GCAATTTTTG	GAAAGCCAAA	GGAGAAGGTA	TACGCCGACG	AGATAGCAAA	AGCCTGGGAA	900
AGTGGAGAGA	ACCTTGAGAG	AGTTGCCAAA	TACTCGATGG	AAGATGCAAA	GGCAACTTAT	960
GAAGTCGGGA	AAGAATTCCT	TCCAATGGAA	ATTCAGCTTT	CAAGATTAGT	TGGACAACCT	1020
TTATGGGATG	TTTCAAGGTC	AAGCACAGGG	AACCTTGTAG	AGTGGTTCTT	ACTTAGGAAA	1080
GCCTACGAAA	GAAACGAAGT	AGCTCCAAAC	AAGCCAAGTG	AAGAGGAGTA	TCAAAGAAGG	1140
CTCAGGGAGA	GCTACACACC	NGGATTCGTT	AAAGAGCCAG	AAAAGGGGTT	GTGGGAAAAC	1200
ATAGTATACC	TAGATTTTAG	AGCCCTATAT	CCCTCGATTA	TAATTACCCA	CAATGTTTCT	1260
CCCGATACTC	TAAATCTTGA	GGGATGCAAG	AACTATGATA	TCGCTCCTCA	AGTAGGCCAC	1320
AAGTTCTGCA	AGGACATCCC	TGGTTTTATA	CCAAGTCTCT	TGGGACATTT	GTTAGAGGAA	1380
AGACAAAAGA	TTAAGACAAA	AATGAAGGAA	ACTCAAGATC	CTATAGAAAA	AATACTCCTT	1440
GACTATAGAC	AAAAAGCGAT	AAAACCTCTA	GCAAATTCTT	TCTACGGATA	TTATGGCTAT	1500
GCAAAAGCAA	GATGGTACTG	TAAGGAGTGT	GCTGAGAGCG	TTACTGCCTG	GGGAAGAAAG	1560
TACATCGAGT	TAGTATGGAA	GGAGCTCGAA	GAAAAGTTTG	GATTTAAAGT	CCTCTACATT	1620
GACACTGATG	GTCTCTATGC	AACTATCCCA	GGAGGAGAAA	GTGAGGAAAT	AAAGAAAAAG	1680
GCTCTAGAAT	TTGTAAAATA	CATAAATTCA	AAGCTCCCTG	GACTGCTAGA	GCTTGAATAT	1740
GAAGGGTTTT	ATAAGAGGGG	ATTCTTCGTT	ACGAAGAAGA	GGTATGCAGT	AATAGATGAA	1800
GAAGGAAAAG	TCATTACTCG	TGGTTTAGAG	ATAGTTAGGA	GAGATTGGAG	TGAAATTGCA	1860
AAAGAACTC	AAGCTAGAGT	TTTGGAGACA	ATACTAAAAC	ACGGAGATGT	TGAAGAAGCT	1920
GTGAGAATAG	TAAAAGAAGT	AATACAAAAG	CTTGCCAATT	ATGAAATTCC	ACCAGAGAAG	1980
CTCGCAATAT	ATGAGCAGAT	AACAAGACCA	TTACATGAGT	ATAAGGCGAT	AGGTCCTCAC	2040
GTAGCTGTTG	CAAAGAAACT	AGCTGCTAAA	GGAGTTAAAA	TAAAGCCAGG	AATGGTAATT	2100
GGATACATAG	TACTTAGAGG	CGATGGTCCA	ATTAGCAATA	GGGCAATTCT	AGCTGAGGAA	2160
TACGATCCCA	AAAAGCACAA	GTATGACGCA	GAATATTACA	TGGAGAACCA	GGTTCTTCCA	2220
GCGGTACTTA	GGATATTGGA	GGGATTTGGA	TACAGAAAGG	AAGACCTCAG	ATACCAAAAG	2280
ACAAGACAAG	TCGGCCTAAC	TTCTTGGCTT	AACATTAAAA	AATCCTAG	2328	

PFU DNA POLYMERASE

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG	ATGTGGATTA	CATAACTGAA	GAAGGAAAAC	CTGTTATTAG	GCTATTCAAA	60
AAAGAGAACG	GAAAATTTAA	GATAGAGCAT	GATAGAACTT	TTAGACCATA	CATTTACGCT	120
CTTCTCAGGG	ATGATTCAAA	GATTGAAGAA	GTTAAGAAAA	TAACGGGGGA	AAGGCATGGA	180
AAGATTGTGA	GAATTGTTGA	TGTAGAGAAG	GTTGAGAAAA	AGTTTCTCGG	CAAGCCTATT	240
ACCGTGTGGA	AACTTTATTT	GGAACATCCC	CAAGATXXXC	CCACTATTAG	AGAAAAAGTT	300
AGAGAACATC	CAGCAGTTGT	GGACATCTTC	GAATACGATA	TTCCATTTGC	AAAGAGATAC	360
CTCATCGACA	AAGGCCTAAT	ACCAATGGAG	GGGGAAGAAG	AGCTAAAGAT	TCTTGCCTTC	420
GCNATAGCNA	CCCTCTATCA	CGAAGGAGAA	GAGTTTGGAA	AAGGCCCAAT	TATAATGATT	480
AGTTATGCAG	ATGAAAATGA	AGCAAAGGTG	ATTACTTGGA	AAAACATAGA	TCTTCCATAC	540
GTTGAGGTTG	TATCAAGCGA	GAGAGAGATG	ATAAAGAGAT	TTCTCAGGAT	TATCAGGGAG	600
AAGGATCCTG	ACATTATAGT	TACTTATAAT	GGAGACTCAT	TCGCATTCCC	ATATTTAGCG	660
AAAAGGGCAG	AAAAACTTGG	GATTAAATTA	ACCATTGGAA	GAGATGGAAG	CGAGCCCAAG	720
ATGCAGAGAA	TAGGCGATAT	GACGGCTGTA	GAAGTCAAGG	GAAGAATACA	TTTCGACTTG	780
TATCATGTAA	TAACAAGGAC	AATAAATCTC	CCAACATACA	CACTAGAGGC	TGTATATGAA	840
GCAATTTTTG	GAAAGCCAAA	GGAGAAGGTA	TACGCCGACG	AGATAGCAAA	AGCCTGGGAA	900

Fig 13A (cont)

AGTGGAGAGA	ACCTTGAGAG	AGTTGCCAAA	TACTCGATGG	AAGATGCAAA	GGCAACTTAT	960
GAACTCGGGA	AAGAATTCCT	TCCAATGGAA	ATTCAGCTTT	CAAGATTAGT	TGGACAACCT	1020
TTATGGGATG	TTTCAAGGTC	AAGCACAGGG	AACCTTGTAG	AGTGGTTCTT	ACTTAGGAAA	1080
GCCTACGAAA	GAAACGAAGT	AGCTCCAAAC	AAGCCAAGTG	AAGAGGAGTA	TCAAAGAAGG	1140
CTCAGGGAGA	GCTACACAGG	TGGATTCGTT	AAAGAGCCAG	AAAAGGGGTT	GTGGGAAAAC	1200
ATAGTATAAC	TAGATTTTAG	AGCCCTATAT	CCCTCGATTA	TAATTACCCA	CAATGTTTCT	1260
CCCGATACTC	TAAATCTTGA	GGGATGCAAG	AACTATGATA	TCGCTCCTCA	AGTAGGCCAC	1320
AAGTTCTGCA	AGGACATCCC	TGGTTTTATA	CCAAGTCTCT	TGGGACATTT	GTTAGAGGAA	1380
AGACAAAAGA	TTAAGACAAA	AATGAAGGAA	ACTCAAGATC	CTATAGAAAA	AATACTCCTT	1440
GACTATAGAC	AAAAAGCGAT	AAAACCTCTTA	GCAAATTCTT	TCTACGGATA	TTATGGCTAT	1500
GCAAAAGCAA	GATGGTACTG	TAAGGAGTGT	GCTGAGAGCG	TTACTGCCTG	GGGAAGAAAG	1560
TACATCGAGT	TAGTATGGAA	GGAGCTCGAA	GAAAAGTTTG	GATTTAAAGT	CCTCTACATT	1620
GACACTGATG	GTCTCTATGC	AACTATCCCA	GGAGGAGAAA	GTGAGGAAAT	AAAGAAAAAG	1680
GCTCTAGAAT	TTGTAAAATA	CATAAATTCA	AAGCTCCCTG	GACTGCTAGA	GCTTGAATAT	1740
GAAGGGTTTT	ATAAGAGGGG	ATTCTTCGTT	ACGAAGAAGA	GGTATGCAGT	AATAGATGAA	1800
GAAGGAAAAG	TCATTACTCG	TGGTTTAGAG	ATAGTTAGGA	GAGATTGGAG	TGAAATTGCA	1860
AAAGAACTC	AAGCTAGAGT	TTTGGAGACA	ATACTAAAAC	ACGGAGATGT	TGAAGAAGCT	1920
GTGAGAATAG	TAAAAGAAGT	AATACAAAAG	CTTGCCAATT	ATGAAATTCC	ACCAGAGAAG	1980
CTCGCAATAT	ATGAGCAGAT	AACAAGACCA	TTACATGAGT	ATAAGGCGAT	AGGTCCTCAC	2040
GTAGCTGTTG	CAAAGAAACT	AGCTGCTAAA	GGAGTTAAAA	TAAAGCCAGG	AATGGTAATT	2100
GGATACATAG	TACTTAGAGG	CGATGGTCCA	ATTAGCAATA	GGGCAATTCT	AGCTGAGGAA	2160
TACGATCCCA	AAAAGCACAA	GTATGACGCA	GAATATTACA	TGGAGAACCA	GGTTCTTCCA	2220
GCGGTACTTA	GGATATTGGA	GGGATTTGGA	TACAGAAAGG	AAGACCTCAG	ATACCAAAAG	2280
ACAAGACAAG	TCGGCCTAAC	TTCTGGCTT	AACATTAAAA	AATCCTAG		2328

KOD DNA POLYMERASE

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTCG	ACACTGACTA	CATAACCGAG	GATGGAAAGC	CTGTCATAAG	AATTTTCAAG	60
AAGGAAAACG	GCGAGTTTAA	GATTGAGTAC	GACCGGACTT	TTGAACCCTA	CTTCTACGCC	120
CTCCTGAAGG	ACGATTCTGC	CATTGAGGAA	GTCAAGAAGA	TAACCGCCGA	GAGGCACGGG	180
ACGGTTGTAA	CGGTTAAGCG	GGTTGAAAAG	GTTCAGAAGA	AGTTCCTCGG	GAGACCAGTT	240
GAGGTCTGGA	AACTCTACTT	TACTCATCCG	CAGGACXXXC	CAGCGATAAG	GGACAAGATA	300
CGAGAGCATC	CAGCAGTTAT	TGACATCTAC	GAGTACGACA	TACCCTTCGC	CAAGCGCTAC	360
CTCATAGACA	AGGGATTAGT	GCCAATGGAA	GGCGACGAGG	AGCTGAAAAT	GCTCGCCTTC	420
GACATTGAAA	CTCTCTACCA	TGAGGGCGAG	GAGTTCGCCG	AGGGGCCAAT	CCTTATGATA	480
AGCTACGCCG	ACGAGGAAGG	GGCCAGGGTG	ATAACTTGGA	AGAACGTGGA	TCTCCCCTAC	540
GTTGACGTCG	TCTCGACGGA	GAGGGAGATG	ATAAAGCGCT	TCCTCCGTGT	TGTGAAGGAG	600
AAAGACCCGG	ACGTTCTCAT	AACCTACAAC	GGCGACAAC	TCGACTTCGC	CTATCTGAAA	660
AAGCGCTGTG	AAAAGCTCGG	AATAAACTTC	GCCCTCGGAA	GGGATGGAAG	CGAGCCGAAG	720
ATTCAGAGGA	TGGGCGACAG	GTTTGCCGTC	GAAGTGAAGG	GACGGATACA	CTTCGATCTC	780
TATCCTGTGA	TAAGACGGAC	GATAAACCTG	CCCACATACA	CGCTTGAGGC	CGTTTATGAA	840
GCCGTCTTCG	GTCAGCCGAA	GGAGAAGGTT	TACGCTGAGG	AAATAACCAC	AGCCTGGGAA	900
ACCGGCGAGA	ACCTTGAGAG	AGTCGCCCGC	TACTCGATGG	AAGATGCGAA	GGTCACATAC	960
GAGCTTGGGA	AGGAGTTCCT	TCCGATGGAG	GCCCAGCTTT	CTCGCTTAAT	CGGCCAGTCC	1020
CTCTGGGACG	TCTCCCGCTC	CAGCACTGGC	AACCTCGTTG	AGTGGTTCTT	CCTCAGGAAG	1080
GCCTATGAGA	GGAATGAGCT	GGCCCCGAAC	AAGCCCGATG	AAAAGGAGCT	GGCCAGAAGA	1140
CGGCAGAGCT	ATGAAGGAGG	CTATGTAAAA	GAGCCCGAGA	GAGGGTTGTG	GGAGAACATA	1200
GTGTACCTAG	ATTTTAGATC	CCTGTACCCC	TCAATCATCA	TCACCCACAA	CGTCTCGCCG	1260
GATACGCTCA	ACAGAGAAGG	ATGCAAGGAA	TATGACGTTG	CCCCACAGGT	CGGCCACCGC	1320
TTCTGCAAGG	ACTTCCCAGG	ATTTATCCCG	AGCCTGCTTG	GAGACCTCCT	AGAGGAGAGG	1380
CAGAAGATAA	AGAAGAAGAT	GAAGGCCACG	ATTGACCCGA	TCGAGAGGAA	GCTCCTCGAT	1440
TACAGGCAGA	GGGCCATCAA	GATCCTGGCA	AACAGCTACT	ACGGTTACTA	CGGCTATGCA	1500
AGGGCGCGCT	GGTACTGCAA	GGAGTGTGCA	GAGAGCGTAA	CGGCCTGGGG	AAGGGAGTAC	1560
ATAACGATGA	CCATCAAGGA	GATAGAGGAA	AAGTACGGCT	TTAAGGTAAT	CTACAGCGAC	1620

Fig 13A (cont)

ACCGACGGAT	TTTTTGCCAC	AATACCTGGA	GCCGATGCTG	AAACCGTCAA	AAAGAAGGCT	1680
ATGGAGTTCC	TCAAGTATAT	CAACGCCAAA	CTTCCGGGCG	CGCTTGAGCT	CGAGTACGAG	1740
GGCTTCTACA	AACGCGGCTT	CTTCGTCACG	AAGAAGAAGT	ATGCGGTGAT	AGACGAGGAA	1800
GGCAAGATAA	CAACGCGCGG	ACTTGAGATT	GTGAGGCGTG	ACTGGAGCGA	GATAGCGAAA	1860
GAGACGCAGG	CGAGGGTTCT	TGAAGCTTTG	CTAAAGGACG	GTGACGTCGA	GAAGGCCGTG	1920
AGGATAGTCA	AAGAAGTTAC	CGAAAAGCTG	AGCAAGTACG	AGGTTCCGCC	GGAGAAGCTG	1980
GTGATCCACG	AGCAGATAAC	GAGGGATTTA	AAGGACTACA	AGGCAACCGG	TCCCCACGTT	2040
GCCGTTGCCA	AGAGGTTGGC	CGCGAGAGGA	GTCAAAATAC	GCCCTGGAAC	GGTGATAAGC	2100
TACATCGTGC	TCAAGGGCTC	TGGGAGGATA	GGCGACAGGG	CGATACCGTT	CGACGAGTTC	2160
GACCCGACGA	AGCACAAGTA	CGACGCCGAG	TACTACATTG	AGAACCAGGT	TCTCCCAGCC	2220
GTTGAGAGAA	TTCTGAGAGC	CTTCGGTTAC	CGCAAGGAAG	ACCTGCGCTA	CCAGAAGACG	2280
AGACAGGTTG	GTTTGAGTGC	TTGGCTGAAG	CCGAAGGGAA	CTTGA	2325	

Vent DNA POLYMERASE

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG	ACACTGATTA	CATAACAAAA	GATGGCAAGC	CTATAATCCG	AATTTTAAAG	60
AAAGAGAACG	GGGAGTTTAA	AATAGAACTT	GACCCTCATT	TTCAGCCCTA	TATATATGCT	120
CTTCTCAAAG	ATGACTCCGC	TATTGAGGAG	ATAAAGGCAA	TAAAGGGCGA	GAGACATGGA	180
AAAACGTGTA	GAGTGCTCGA	TGCAGTGAAA	GTCAGGAAAA	AATTTTGGG	AAGGGAAGTT	240
GAAGTCTGGA	AGCTCATTTT	CGAGCATCCC	CAAGACXXXC	CAGCTATGCG	GGGCAAAATA	300
AGGGAACATC	CAGCTGTGGT	TGACATTTAC	GAATATGACA	TACCCTTTGC	CAAGCGTTAT	360
CTCATAGACA	AGGGCTTGAT	TCCCATGGAG	GGAGACGAGG	AGCTTAAGCT	CCTTGCCTTT	420
GATATTGAAA	CGTTTTATCA	TGAGGGGAGAT	GAATTTGGAA	AGGGCGAGAT	AATAATGATT	480
AGTTATGCCG	ATGAAGAAGA	GGCCAGAGTA	ATCACATGGA	AAAATATCGA	TTTGCCGTAT	540
GTCGATGTTG	TGTCCAATGA	AAGAGAAATG	ATAAAGCGTT	TTGTTCAAGT	TGTTAAAGAA	600
AAAGACCCCG	ATGTGATAAT	AACTTACAAT	GGGGACAATT	TTGATTTGCC	GTATCTCATA	660
AAACGGGCAG	AAAAGCTGGG	AGTTCGGCTT	GTCTTAGGAA	GGGACAAAGA	ACATCCCGAA	720
CCCAAGATTC	AGAGGATGGG	TGATAGTTTT	GCTGTGGA	TCAAGGGTAG	AATCCACTTT	780
GATCTTTTCC	CAGTTGTGCG	AAGGACGATA	AACCTCCCAA	CGTATACGCT	TGAGGCAGTT	840
TATGAAGCAG	TTTTAGGAAA	AACCAAAAGC	AAATTAGGAG	CAGAGGAAAT	TGCCGCTATA	900
TGGGAAACAG	AAGAAAGCAT	GAAAAAACTA	GCCCAGTACT	CAATGGAAGA	TGCTAGGGCA	960
ACGTATGAGC	TCGGGAAGGA	ATTCTTCCCC	ATGGAAGCTG	AGCTGGCAAA	GCTGATAGGT	1020
CAAAGTGTAT	GGGACGTCTC	GAGATCAAGC	ACCGGCAACC	TCGTGGAGTG	GTATCTTTTA	1080
AGGGTGGCAT	ACGCGAGGAA	TGAACCTTGA	CCGAACAAAC	CTGATGAGGA	AGAGTATAAA	1140
CGGCGCTTAA	GAACAACTTA	CCTGGGAGGA	TATGTAAAAG	AGCCAGAAAA	AGGTTTGTGG	1200
GAAAATATCA	TTTATTTGGA	TTTCCGCAGT	CTGTACCCTT	CAATAATAGT	TACTCACAAC	1260
GTATCCCCAG	ATACCCTTGA	AAAAGAGGGC	TGTAAGAATT	ACGATGTTGC	TCCGATAGTA	1320
GGATATAGGT	TCTGCAAGGA	CTTTCCGGGC	TTTATTCCCT	CCATACTCGG	GGACTTAATT	1380
GCAATGAGGC	AAGATATAAA	GAAGAAAATG	AAATCCACAA	TTGACCCGAT	CGAAAAGAAA	1440
ATGCTCGATT	ATAGGCAAAG	GGCTATTAAA	TTGCTTGCAA	ACAGCTATTA	CGGCTATATG	1500
GGGTATCCTA	AGGCAAGATG	GTACTCGAAG	GAATGTGCTG	AAAGCGTTAC	CGCATGGGGG	1560
AGACACTACA	TAGAGATGAC	GATAAGAGAA	ATAGAGGAAA	AGTTCGGCTT	TAAGGTTCTT	1620
TATGCGGACA	CTGACGGCTT	TTATGCCACA	ATACCCGGGG	AAAAGCCTGA	ACTCATTA	1680
AAGAAAGCCA	AGGAATTCCT	AACTACATA	AACTCCAAAC	TTCCAGGTCT	GCTTGAGCTT	1740
GAGTATGAGG	GCTTTTACTT	GAGAGGATTC	TTTGTTACAA	AAAAGCGCTA	TGCAGTCATA	1800
GATGAAGAGG	GCAGGATAAC	AACAAGGGGC	TTGGAAGTAG	TAAGGAGAGA	TTGGAGTGAG	1860
ATAGCTAAGG	AGACTCAGGC	AAAGGTTTTA	GAGGCTATAC	TAAAGAGGGG	AAGTGTTGAA	1920
AAAGCTGTAG	AAGTTGTTAG	AGATGTTGTA	GAGAAAATAG	CAAAATACAG	GGTTCCACTT	1980
GAAAAGCTTG	TTATCCATGA	GCAGATTACC	AGGGATTTAA	AGGACTACAA	AGCCATTGGC	2040
CCTCATGTGC	CGATAGCAAA	AAGACTTGCC	GCAAGAGGGA	TAAAAGTGAA	ACCGGGCACA	2100
ATAATAAGCT	ATATCGTTCT	CAAAGGGAGC	GGAAAGATAA	GCGATAGGGT	AATTTTACTT	2160
ACAGAATACG	ATCCTAGAAA	ACACAAGTAC	GATCCGGACT	ACTACATAGA	AAACCAAGTT	2220
TTGCCGGCAG	TACTTAGGAT	ACTCGAAGCG	TTTGGATACA	GAAAGGAGGA	TTTAAGGTAT	2280
CAAAGCTCAA	AACAAACCGG	CTTAGATGCA	TGGCTCAAGA	GGTAG	2325	

Fig 13A (cont)

Deep Vent

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG	ACGCTGACTA	CATCACCGAG	GATGGGAAGC	CGATTATAAG	GATTTTCAAG	60
AAAGAAAACG	GCGAGTTTAA	GGTTGAGTAC	GACAGAAACT	TTAGACCTTA	CATTTACGCT	120
CTCCTCAAAG	ATGACTCGCA	GATTGATGAG	GTTAGGAAGA	TAACCGCCGA	GAGGCATGGG	180
AAGATAGTGA	GAATTATAGA	TGCCGAAAAG	GTAAGGAAGA	AGTTCCTGGG	GAGGCCGATT	240
GAGGTATGGA	GGCTGTACTT	TGAACACCCT	CAGGACXXXC	CCGCAATAAG	GGATAAGATA	300
AGAGAGCATT	CCGCAGTTAT	TGACATCTTT	GAGTACGACA	TTCCGTTTCG	GAAGAGGTAC	360
CTAATAGACA	AAGGCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGGCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCCAAAGTC	ATAACGTGGA	AAAAGATCGA	TCTCCCGTAC	540
GTGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	600
AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCAAAG	720
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAGAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAAGG	GACTGGAGAG	AGTTGCAAAG	TATTCAATGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACCTTGGTG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCA	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAACTGGAG	GAAAAGTTTC	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCCCT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTTCGT	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAAGATAG	TTAAGGAGGT	AAGTGAAGAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAGTAA		2328

JDF-3

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCA
GGATTGAATACGACCGCGAGTTCGAGCCCTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAA
GATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAAAAAGTTCTCGGCAGGTCT
GTGGAGGTCTGGGTCTCTACTTCACGCACCCGACGAGACXXXCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGG
TCATCGACATCTACGAGTACGACATAACCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGA
GGAAGAGCTTAAACTCATGTCTTCTGACATCGAGACGCTCTACCACGAGGGAGAAGAGTTTGAACCGGGCCGATTCTG
ATGATAAGCTACGCCGATGAAAGCGAGGCGCGGTGATAACCTGGAAGAAGATCGACCTTCTTACGTTGAGGTTGTCT
CCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATAACAACG

19/186

Fig 13A (cont)

CGACAACCTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTTACCCTCGGGAGGGACGGGAGC
GAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCA
TAAGGCGCACCATAAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTTCGGCAAGCCCAAGGAGAAGGT
CTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTGAGAGGGTCGCGCGCTACTCGATGGAGGACGCG
AGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGG
ACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCCTCCTAAGGAAGGCCTACGAGAGGAACGAACCTCGCTCC
CAACAAGCCCGACGAGAGGGAGCTGGCGAGGAGAAGGGGGGGCTACg_cCGGTGGCTACGTCAAGGAGCCGGAGCGGGGA
CTGTGGGACAATATCGTGTATCTAGACTTTTCGTAGTCTCTAC[CCT]TCAATCATAATCACCCACAACGTCTCGCCAGATA
CGCTCAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCCCGAGGTTCGGTCACAAGTTCTGCAAGGACTTCCCCGGCTT
CATTCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTG
GAGAAGAATCTCCTCGATTACAGGCAACGC[GCC]ATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATGCCA
GGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGA
GCTTGAGGAAAAGTTCGGTTTTTAAAGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCT
GAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACCTGCCCGGCCTTCTCGAACTCGAATACG
AGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCG
CGGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGACGCAGGCGAGGGTTTTGGAGGCGATACTCAGG
CACGGTGACGTTGAAGAGGCCGTCAGAATTGTCAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGGAGA
AGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAg_cG
TTTGGCCGCCAGAGGTGTTAAAATCCGGCCCCGGAACCTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGC
GACAGGGCGATTCCCTTCGACGAGTTGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTC
TGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCCG
GCTTGGCGCGTGGCTGAAGCCGAAGGGGAAGAAGAAGTGA

Figure 13B

>Pfu V93R

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVBREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVSSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAI FGKPKKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TGGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPPKKHKYDAEYYIENQVLPVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKs //

>Pfu V93E

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVBREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVSSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAI FGKPKKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TGGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPPKKHKYDAEYYIENQVLPVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKs

>Pfu V93R/G387P

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVBREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVSSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAI FGKPKKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TPGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPPKKHKYDAEYYIENQVLPVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKs

>Pfu V93R/D141A/E143A

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVBREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVSSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAI FGKPKKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TGGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPPKKHKYDAEYYIENQVLPVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKs

>Pfu V93E/G387P

21/186

Fig. 13B (cont)

MILDVDYITEEGKPVIRLFFKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHKGKIVRIVDVEKVEKKFLG
 KPITVWKLYLEHPQDEPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
 GPIIMISYADENEAKVITWKNIDLPYVEVVSSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
 IGRDGSEPKMQRIGDMTAVEVKGRIFHDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYAIDEIAKAWESGENLERV
 AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
 TPGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
 KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
 IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
 SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
 IKPGMVIGYIVLRGDGPISNRAILAEEDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
 NIKKS

>Pfu V93E/D141A/E143A

MILDVDYITEEGKPVIRLFFKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHKGKIVRIVDVEKVEKKFLG
 KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
 GPIIMISYADENEAKVITWKNIDLPYVEVVSSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
 IGRDGSEPKMQRIGDMTAVEVKGRIFHDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYAIDEIAKAWESGENLERV
 AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
 TGGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
 KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
 IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
 SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
 IKPGMVIGYIVLRGDGPISNRAILAEEDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
 NIKKS

>DEEP VENT V93R

MILDADYITEDGKPIIRIFKKENGFEKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHKGKIVRIIDAOKVRKKFLG
 RPIEVWRLYFEHPQDRPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
 GPIIMISYADEEEAKVITWKKIDLPYVEVVSSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLP
 LGRDGSEPKMQRLGDMTAVEIKGRIFHDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWETGKGLERV
 AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSSTGNLVEWYLLRKAYERNELAPNKPDEREYERRRLRESY
 AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLLKRLLLDERQ
 EIKRKMASKDPIEKKMLDYRQRAIKILANSYYGYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
 IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLEIVRRDW
 SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
 VRPGMVIGYIVLRGDGPISKRAILAEEDLRKHKYDAEYYIENQVLPAVLRILEAFGYRKEDLRWQKTKQTGLTAWL
 NIKKK

>DEEP VENT V93E

MILDADYITEDGKPIIRIFKKENGFEKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHKGKIVRIIDAOKVRKKFLG
 RPIEVWRLYFEHPQDEPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
 GPIIMISYADEEEAKVITWKKIDLPYVEVVSSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLP
 LGRDGSEPKMQRLGDMTAVEIKGRIFHDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWETGKGLERV
 AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSSTGNLVEWYLLRKAYERNELAPNKPDEREYERRRLRESY
 AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLLKRLLLDERQ
 EIKRKMASKDPIEKKMLDYRQRAIKILANSYYGYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
 IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLEIVRRDW
 SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
 VRPGMVIGYIVLRGDGPISKRAILAEEDLRKHKYDAEYYIENQVLPAVLRILEAFGYRKEDLRWQKTKQTGLTAWL
 NIKKK

>TGO V93R

MILDTDYITEDGKPVIRIFKKENGFEKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLG
 RPIEVWKLIFYTHPQDRPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
 GPILMISYADEEGARVITWKNIDLPYVDVVSTEEKEMIKRFLKVVKEDPDVLITYNGDNFDFAYLKKRSEKLGVKFI

Fig 13B (cont)

LGREGSEP KIQRMGDRFAVEVKGR IHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAE EIAQAWETGEGLERV
 ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
 GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSL LGDLLEERQK
 VKKKMKATIDPIEKKLLDYRQRAIKILANSFYGYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
 DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
 EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKI
 RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLGAWLK
 PKT

>TGO V93E

MILDTDYITEDGKPVIRIFKKENGEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLG
 RPIEVWKLYFTHPQDEPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
 GPILMISYADEEGARVITWKNIDLPYVDVSTEKEMIKRFLKVVKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
 LGREGSEP KIQRMGDRFAVEVKGR IHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAE EIAQAWETGEGLERV
 ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
 GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSL LGDLLEERQK
 VKKKMKATIDPIEKKLLDYRQRAIKILANSFYGYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
 DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
 EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKI
 RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLGAWLK
 PKT

>KOD V93R

MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
 RPVEVWKLYFTHPQDRPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
 GPILMISYADEEGARVITWKNVDLPYVDVSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINF A
 LGRDGSEP KIQRMGDRFAVEVKGR IHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAE EITPAWETGENLERV
 ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
 GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSL LGDLLEERQK
 IKKKMKATIDPIERKLLDYRQRAIKILANSYGYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFVKVIYS
 DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
 EIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLVIHEQITRDLKDYKATGPHVAVAKRLAARGVKI
 RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLSAWLK
 PKGT

>KOD V93E

MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
 RPVEVWKLYFTHPQDEPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
 GPILMISYADEEGARVITWKNVDLPYVDVSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINF A
 LGRDGSEP KIQRMGDRFAVEVKGR IHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAE EITPAWETGENLERV
 ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
 GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSL LGDLLEERQK
 IKKKMKATIDPIERKLLDYRQRAIKILANSYGYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFVKVIYS
 DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
 EIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLVIHEQITRDLKDYKATGPHVAVAKRLAARGVKI
 RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLSAWLK
 PKGT

>VENT V93R

MILDTDYITKDGP IIRIFKKENGEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHKGKTVRVLDVAVKVRKKFLG
 REVEVWKLI FEHPQDRPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEF GK
 GEIIMISYADEEEARVITWKNIDLPYVDVVSNEREMIKRFVQVVKEDPDV IITYNGDNFDFLYLIKRAEKLGVRLV
 LGRDKEHPEPKIQRMGDSFAVEIKGR IHFDLFPVVRRTINLPTYTLEAVYEA VLGKTKSKLGAE EIAAIWETEESMK

23/186

Fig 13.B (cont)

KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSIILGDLIAM
RQDIKKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGFIYATIPGEKPELIKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIEHQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYIENQVLPVLRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>VENT V93E

MILDTDYITKDGPPIIRIFKKENGFEKIELDPHFQPIYIALLKDDSAIEEIKAIKGERHKGKTVRVLDVAVKVRKKFLG
REVEVWKLIFEHPQDEPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFKG
GEIIMISYADEEEARVITWKNIDLPHYVDVVSNEREMIKRFVQVVEKDPDVIITYNGDNFDLPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRRTINLPTYTLEAVYEAVLGKTKSKLGAEETIAAIWETEEESMK
KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSIILGDLIAM
RQDIKKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGFIYATIPGEKPELIKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIEHQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYIENQVLPVLRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>JDF-3 V93R

MILDVDYITENGKPVIRVFKKENGFEFRIEYDREFEPYFYALLRDDSIAIEEIKKITAERHGRVVKVKRAEKVKKKFLGR
SVEVWVLYFTHPQDRPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSF[D]I[ET]LYHEGEEFGTGP
ILMISYADESEARVITWKKIDLPHYVEVVSTEKEMIKRFLRVVVEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR
DGSEPDKIQRMGDRFAVEVKGRVHFDLPHYVIRRTINLPTYTLEAVYEAVFGKPKVKYAEETIATAWETGEGLERVARYS
MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGYAGGYVK
EPERGLWDNIVYLDFRSLY[P]SIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLGNNLEERQKIKRKM
ATLDPLEKNLLDYRQR[A]IKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA
TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQA
RVLEAILRHGDVEEAVRIVREVTEKLSKYEPPEKLVIEHQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI
VLKGSGRIGDRAIPFDEFDPTKHKYDADYIENQVLPVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

>JDF-3 V93E

MILDVDYITENGKPVIRVFKKENGFEFRIEYDREFEPYFYALLRDDSIAIEEIKKITAERHGRVVKVKRAEKVKKKFLGR
SVEVWVLYFTHPQDEPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSF[D]I[ET]LYHEGEEFGTGP
ILMISYADESEARVITWKKIDLPHYVEVVSTEKEMIKRFLRVVVEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR
DGSEPDKIQRMGDRFAVEVKGRVHFDLPHYVIRRTINLPTYTLEAVYEAVFGKPKVKYAEETIATAWETGEGLERVARYS
MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGYAGGYVK
EPERGLWDNIVYLDFRSLY[P]SIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLGNNLEERQKIKRKM
ATLDPLEKNLLDYRQR[A]IKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA
TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQA
RVLEAILRHGDVEEAVRIVREVTEKLSKYEPPEKLVIEHQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI
VLKGSGRIGDRAIPFDEFDPTKHKYDADYIENQVLPVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

Fig. 14-1

5' ATG ATC CTC GAT ACA GAC TAC ATA ACT GAG GAT GGA AAG CCC GTC ATC 48
 TAC TAG GAG CTA TGT CTG ATG TAT TGA CTC CTA CCT TTC CCG CAC TAG 48
 M I L D T D Y I T E D G R P V I 16
 ACG ATC TTC AAG AAG GAG AAC GGC GAG TTC ACC ATA GAC TAC GAC AGA 96
 TCC TAG AAG TTC TTC CTC TTG CCG CTC AAG TGG TAT CTG ATG CTG TCT 96
 R I F K K E N G E F T I D Y D R 32
 AAC TTT GAG CCA TAC ATC TAC GCG CTC TTG AAG GAC GAC TCT CCG ATT 144
 TTG AAA CTC GGT ATG TAG ATG CCG GAG AAC TTC CTC CTG AGA GGC TAA 144
 N F E P Y I Y A L L K D D S P I 48
 GAG GAC GTC AAG AAG ATA ACT GCC GAG AGG CAC CCG ACT ACC GTT AGG 192
 CTC CTG CAG TTC TTC TAT TGA CCG CTC TCC GTC CCG TGA TGG CAA TCC 192
 E D V K K I T A E R H G T T V R 64
 GTT GTC AGG GCC GAG AAA GTG AAG AAG AAG TTC CTA GGC AGC CCG ATA 240
 CAA CAG TCC CCG CTC TTT CAC TTC TTC TTC AAG GAT CCG TCC GGC TAT 240
 V V R A E K V K K K F L G R P I 80
 GAG GTC TGG AAG CTC TAC TTC ACT CAC CCC CAG GAC NNN CCC GCA ATC 288
 CTC CAG ACC TTC GAG ATG AAG TGA GTG GCG CTC CTG GCG CGT TAG 288
 E V W K L Y F T H P Q D P A I 96

Tgo 93 NNN = AGA, AGG, CGA, CCG, CGG, CGT (R)
 GAA, GAG (E)

25/186

Fig. 14-2

AGG GAC AAG ATA AAG GAG CAT CCT GCC GTT GTG GAC ATC TAC GAG TAC 336
 TCC CTG TTC TAT TTC CTC GTA GGA CGG CAA CAC CTG TAG ATG CTC ATG 836
 R D K I K E H F A V V D I Y E Y 112

 GAC ATC CCC TTC GCG AAG CGC TAC CTC ATA GAC AAA GCG TTA ATC CCG 384
 CTG TAG GGG AAG CCC TTC GCG ATG GAG TAT CTG TTT CCG AAT TAC GGC 384
 D I F F A K R Y L I D K G L I F 128

 ATG GAC GCC GAC GAG GAA CTT AAG ATG CTC GCC TTC GAC ATC GAG ACG 432
 TAC CTC CCG CTG CTC CTT GAA TTC TAC GAG CGG AAG CTG TAG CTC TGC 432
 M E C D E E L K M L A F D I E T 144

 CTC TAT CAC GAG CGC GAG GAG TTC GCC GAA GGG CCT ATC CTG ATG ATA 480
 GAG ATA GTG CTC CCG CTC CTC AAG CGG CTT CCC GGA TAG GAC TAC TAT 480
 L Y H E G E E F A E G P I L M I 160

 AGC TAC GCC GAC GAG GAA GGG GCG CGC GTT ATT ACC TGG AAG AAT ATC 528
 TCG ATG CGG CTG CTC CTT CCC CGC GCG CAA TAA TGG ACC TTC TTA TAG 528
 S Y A D E E G A R V I T W K N I 176

 GAC CTT CCC TAT GTC GAC GTC GTT TCC ACC GAG AAG GAG ATG ATA AAG 576
 CTG GAA GGG ATA CAG CTG CAG CAA AGG TGG CTC TTC CTC TAC TAT TTC 576
 D L F Y V D V V S T E K E M I K 192

 CGC TTC CTC AAG GTC GTC AAG GAA AAG GAT CCC GAC GTC CTC ATA ATC 624
 GCG AAG GAG TTC CAG CAG TTC CTT TTC CTA GGG CTG CAG GAG TAT TAG 624
 R F L K V V K E K D P D V L I I 208

26/186

Fig 14-3

TAC AAC GGC GAC AAC TTC GAC TTC GCC TAC CTC AAG AAG CGC TCC GAC 672
 ATG TTG CCG CTG TTG AAG CTG AAG CGG ATG GAG TTC TTC GCG AGG CTC 672
 Y N G D N F D F A Y L K K R S E 224
 AAG CTC GGA GTC AAG TTC ATC CTC GGA AAG GAA GGG AGC GAA CCG AAA 720
 TTC GAG CCG CAG TTC AAG TAG GAG CCG TCC CTT CCC TCG CTT GGC TTT 720
 K L G V K F I L G R E G S E F K 240
 ATC CAG CGC ATC GCC GAT CGC TTT GCG GTG GAG CTC AAG GGA AGG ATT 768
 TAG GTC GCG TAC CCG CTA GCG AAA GCG CAG CTC CAG TTC CCG TCC TAA 768
 I Q R M G D R F A V E V K G R I 256
 CAC TTC GAC CTC TAC CCG GTC ATT AAG AGA ACG ATT AAC CTC CCC ACT 816
 GTG AAG CTG GAG ATG GGG CAG TAA TCC TCT TGC TAA TTG GAG GCG TGA 816
 H F D L Y P V I R R T I N L F T 272
 TAC ACC CTT GAG GCA GTA TAT GAA GCC ATC TTT GGA CAG CCG AAG GAG 864
 ATG TGG GAA CTC CGT CAT ATA CTT CGG TAG AAA CCG GTC GGC TTC CTC 864
 Y T L E A V Y E A I F G Q E K E 288
 AAG GTC TAC CCG CAG GAG ATA GCG CAG GCC TGG GAA ACG GCG GAG GGA 912
 TTC CAG ATG CGA CTC CTC TAT CCG GTC CCG ACC CTT TGC CCG CTC CCG 912
 K V Y A E E I A Q A W E T G E G 304
 TTA GAA AAG GTG GCC CCG TAC TCG ATG GAG GAC GCG AAG GAA ACC TAT 960
 AAT CTT TCC CAG CCG GCG ATG AGC TAG CTC CTG CCG TTC CAT TGG ATA 960
 L E R V A R Y S M E D A K V T Y 320

27/186

Fig 14-4

GAA CTC GGA AAA GAG TTC TTC CCT ATG GAA GCC CAG CTC TCG CGC CTC	1008
CTT GAG CCT TTT CTC AAG AAG GGA TAC CTT CGG GTC GAG AGC GCG GAG	1008
E L G K E P F F M E A Q L S R L	336
GTA GGC CAG AGC CTC TGG GAT GEA TCT CGC TCG AGT ACC GGA AAC CTC	1036
CAT CCG GTC TCG GAG ACC CTA CAT AGA GCG AGC TCA TGG CCT TTG GAG	1036
V G Q S L W D V S R S S T G N L	352
GTC GAG TGG TTT TTG CTG AGG AAG GCC TAC GAG AGG AAT GAA CTT GCA	1104
CAG CTC ACC AAA AAC GAC TCC TTC CGG ATG CTC TCC TTA CTT GAA CGT	1104
V E W F L L R K A Y E R N E L A	368
CCA AAC AAG CCG GAC GAG AGC GAG CTG GCA AGA ACA AGG GAG AGC TAC	1152
GGT TTG TTC GGC CTG CTC TCC CTC GAC CGT TCT TCT TCC CTC TCG ATG	1152
P N K P D E R E L A R R R E S Y	384
GCG GGT GGA TAC GTC AAG GAG CCC GAA AGG TGA CTC TGG GAG AAC ATC	1200
CGC CCA CCT ATG CAG TTC CTC GGG CTT TCC CCT GAC ACC CTC TTG TAG	1200
A G G Y V K E P E R G L W E N I	400
GTG TAT CTG GAC TTC CGC TCC CTG TAT CCT TCG ATA ATA ATC ACC CAT	1248
CAC ATA GAC CTG AAG GCG AGG GAC ATA GGA AGC TAT TAT TAG TGG GTA	1248
V Y L D F R S L Y P S I I I T H	416
AAC GTC TCC CCT GAT ACA CTC AAC AGG GAG GGT TGT GAG GAG TAC GAC	1296
TTG CAG AGG GGA CTA TGT GAG TTG TCC CTC CCA ACA CTC CTC ATG CTG	1296
N V S P D T L N R E G C E E Y D	432

28/186

Fig. 14-5

GTG GGT CCT CAG ATA GGC CAT AAG TTC TGC AAG GAC TTC CCC GGC TTC	1344
CAC CGA GGA GTC CAT CCG GGA TTC AAG ACG TTC CTG AAG GGG CCG AAG	1344
V A P Q V G H K F C K D F P G F	448
ATC CCA AGC CTC CTC GGA GAC CTC TTG GAG GAG ACA CAG AAG GTA AAG	1392
TAG GGT TCG GAG GAG CCT CTG GAG AAC CTC CTC TGT GTC TTC CAT TTC	1392
I P S L L G D L L E E R Q K V K	454
AAG AAG ATG AAG GCC ACT ATA GAC CCA ATC GAG AAG AAA CTC CTC GAT	1440
TTC TTC TAC TTC CCG TGA TAT CTG GGT TAG CTC TTC TTT GAG GAG CTA	1440
K K M K A T I D P I E K K L L D	480
TAC AGG CAA CGA CCA ATC AAA ATC CTT GCT AAT AGC TTC TAC GGT TAC	1488
ATG TCC GTT GCT CGT TAG TTT TAG GAA CGA TTA TCG AAG ATG CCA ATG	1488
Y R Q R A I K I L A N S F Y G Y	496
TAC GGC TAT ACA AAG GCC CGC TGG TAC TAC AAG GAG TGC GCC GAG AGC	1536
ATG CCG ATA TGT TTC CCG GCG ACC ATG ATG TTC CTC ACC CCG CTC TCG	1536
Y G Y T K A R W Y Y K E C A E S	512
GTT ACC GGT TCG GGC AGG GAG TAC ATC GAG ACC ACG ATA AGG GAA ATA	1584
CAR TGG CCA ACC CCG TCC CTC ATG TAG CTC TGG TGC TAT TCC CTT TAT	1584
V T G W G R E Y I E T T I R E I	528
GAG GAG AAA TTT GGC TTT AAA GTC CTC TAC GCG GAC ACA GAT GGA TTT	1632
CTC CTC TTT AAA CCG AAA TTT CAG GAG ATG CCG CTG TGT CTA COT AAA	1632
E E K F G F K V L Y A D T D G F	544
TTC GCA ACA ATA CCT GGA GCG GAC GCC GAA ACC GTC AAA AAG AAG GCA	1680
AAG CGT TGT TAT GGA CCT CGC CTG CCG CTT TGG CAG TTT TTC TTC CGT	1680
F A T I F G A D A E T V K K K A	560

29/186

Fig 14-6

AAG GAG TTC CTG GAC TAC ATC AAC GCC AAA CTG CCC GGC CTG CTC GAA 1728
TTC CTC AAG GAC CTG ATG TAG TTG CCG TTT GAC GGG CCG GAC GAG CTT 1728
K E F L D Y I N A K L P G L L E 576

CTC GAA TAC GAG GGC TTC TAC AAG CGC GGC TTC TTC GTG ACG AAG AAG 1776
GAG CTT ATG CTC CCG AAG ATG TTC GCG CCG AAG AAG CAC TGC TTC TTC 1776
L E Y E G F Y K R C F F V T K K 592

AAG TAC GCG GTT ATA GAC GAG GAG GAC AAG ATA ACG ACG CGC GGG CTT 1824
TTC ATG CCG CAA TAT CTG CTC CTC CTG TTC TAT TGC TGC GCG CCC GAA 1824
K Y A V I D E E D K I T T R G L 608

GAA ATA GTT AGG CGT GAC TGG AGC GAG ATA CCG AAG GAG ACG CAG GCG 1872
CTT TAT CAA TCC GCA CTG ACC TCG CTC TAT CCG TTC CTC TGC GTC CGC 1872
E I V R R D W S E I A K E T Q A 624

AGG GTT CTT CAG GCG ATA CTA AAG CAC GGT GAC GTT GAA GAA GCG GTA 1920
TCC CAA GAA CTC CGC TAT GAT TTC GTG CCA CTG CAA CTT CTT CGC CAT 1920
R V L E A I L K H G D V E E A V 640

AGG ATT GTC AAA GAG GTT ACG GAG AAG CTG ACC AAG TAC GAG GTT CCA 1968
TCC TAA CAG TTT CTC CAA TGC CTC TTC GAC TCG TTC ATG CTC CAA GGT 1968
R I V K E V T E K L S K Y E V P 656

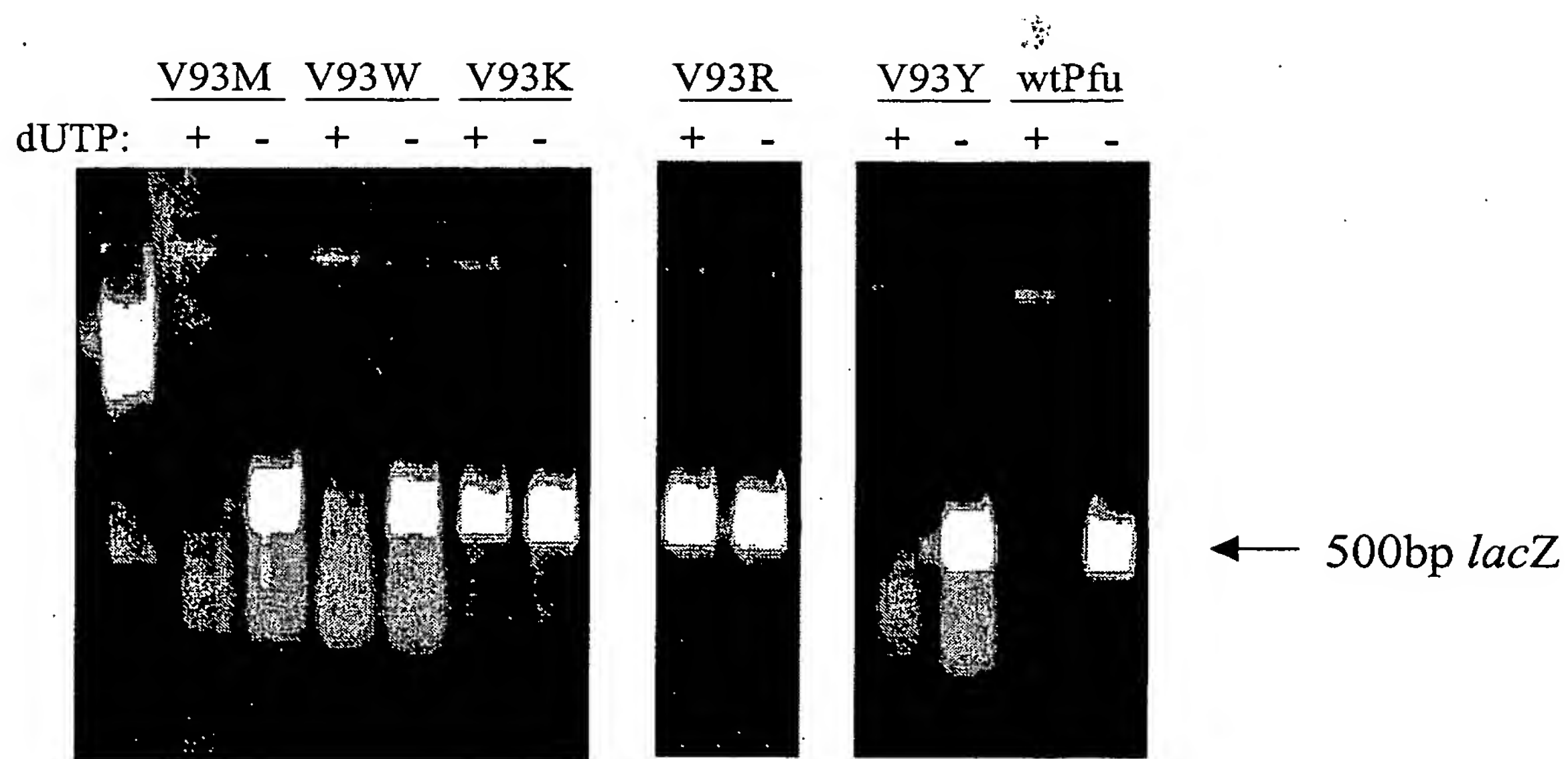
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GGC CTC TTC GAC CAG TAG ATG CTC GTC TAT TGC GCG CTG GAC TTC CTG 2016
F E K L V I Y E Q I T R D L K D 672

30/186

Fig. 14-7

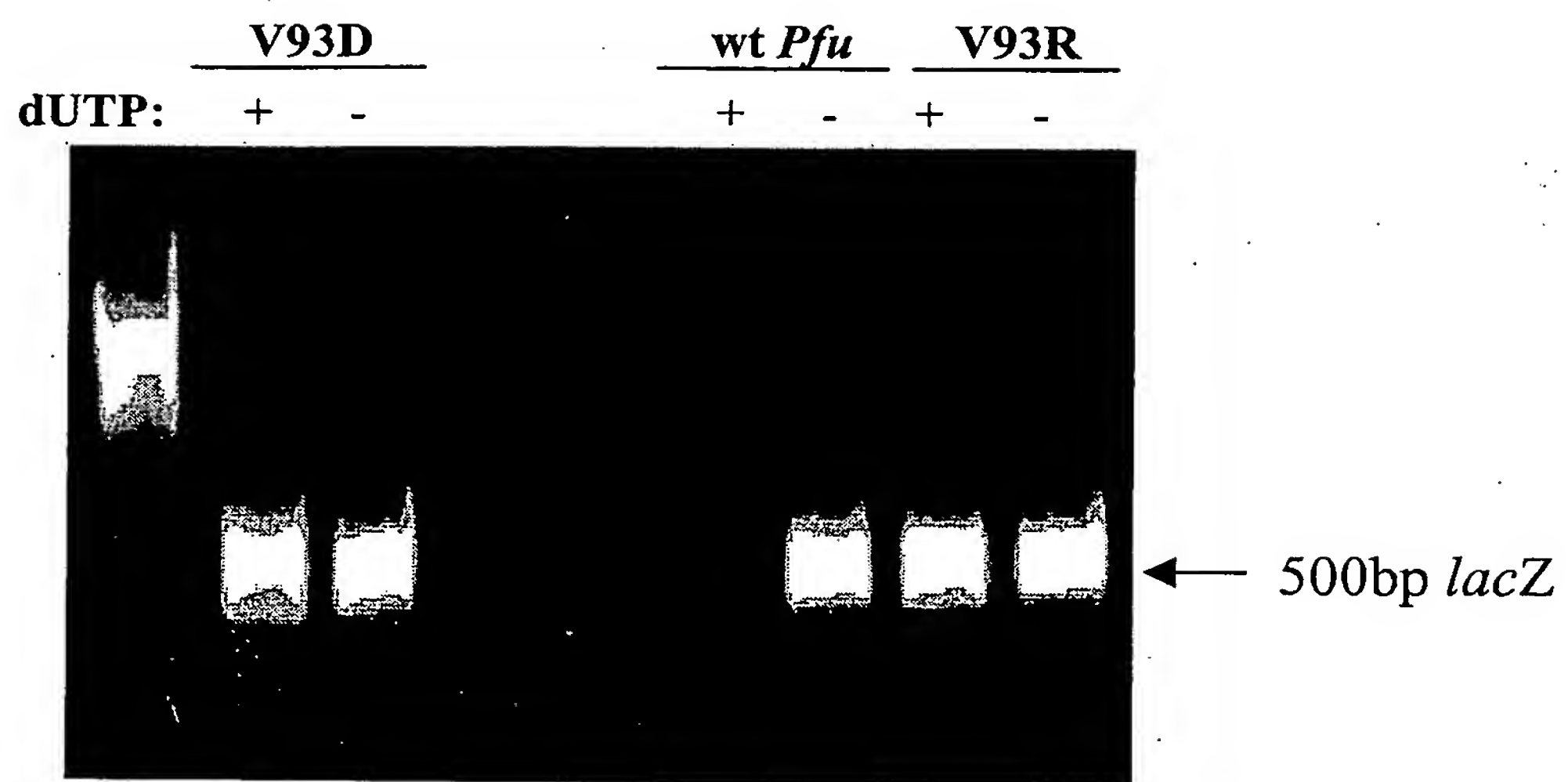
TAC AAG GCC ACC GGG CCG CAT GTG GCT GTT GCA AAA CGC CTC GCC GCA	2064
ATG TTC CGG TGG CCC GGC GTA CAG CGA CAA CGT TTT GCG GAG CGG CGT	2064
Y K A T G P H V A V A K R L R A	698
AGG GGC ATA AAA ATC CGG CCC GGA ACG GTC ATA AGC TAC ATC GTG CTC	2112
TCC CCC TAT TTT TAG GCC GGG CCT TGC CAG TAT TCG ATG TAG CAC GAG	2112
R G I K I R P G T V I S Y I V L	704
AAA GGC TCG GGA AGG ATT GGG GAC AGG GCT ATA CCC TTT GAC GAA TTT	2160
TTT CCG AGC CCT TCG TAA CCG CTG TCC CGA TAT GGG AAA CTG CTT AAA	2160
K G S G R I G D R A I P F D E F	720
GAC CCG GCA AAG CAC AAG TAC GAT GCA GAA TAC TAC ATC GAG AAC CAG	2208
CTG GGC CGT TTC GTG TTC ATG CTA CGT CTT ATG ATG TAG CTC TTG GTC	2208
D P A K H K Y D A E Y Y I E N Q	736
GTT CTT CCA GCT GTG GAG AGG ATT CTG AGG GCC TTT GGT TAC CGT AAA	2256
CRA GAA GGT CGA CAC CTC TCC TAA GAC TCC CGG AAA CCA ATG GCA TTT	2256
V L F R V E R I L R A F G Y R K	752
GAA GAT TTA AGG TAT CAG AAA ACG CCG CAG GTT GGC TTG GGG CCG TGG	2304
CTT CTA AAT TCC ATA GTC TTT TGC GCC GTC CAA CCG AAC CCC CGC ACC	2304
E D L R Y Q K T R Q V G L G A W	768
CTA AAA CCT AAG ACA TGA	2322
GAT TTT GGA TTC TGT ACT	2322
L K P K T *	773

31/186



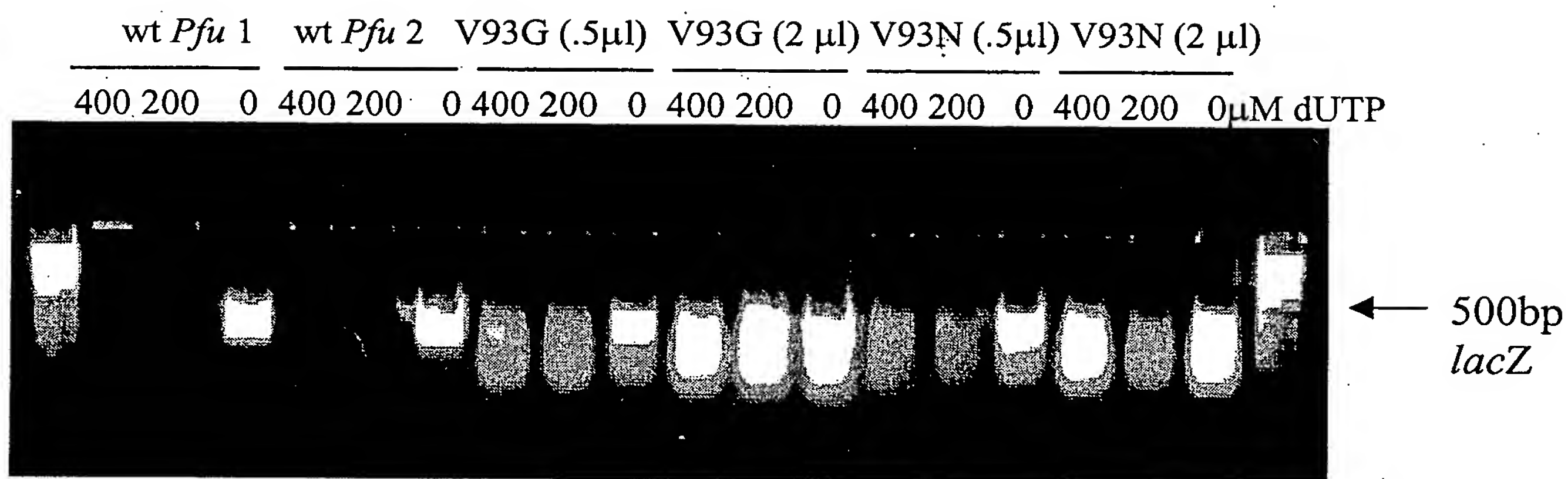
Results: *Pfu* V93K and V93R mutants show significantly improved dUTP incorporation compared to wild type *Pfu*. In contrast, the *Pfu* V93W, V93Y, and V93M mutants show little-to-no improvement in dUTP incorporation.

Figure 15A



Results: The *Pfu* V93D and V93R mutants show significantly improved dUTP incorporation compared to wild type *Pfu*.

Figure 15B



Results: The *Pfu* V93N mutant shows a very small improvement in dUTP incorporation compared to wild type *Pfu*. In contrast, the *Pfu* V93G mutant shows little-to-no improvement.

Figure 15C

34/186

Figure 16: Polymerase activity and Temperature optimum of Pfu N terminal truncation mutants

Pfu clone #	Truncated after Pfu residue	Relative DNA polymerase activity	Temperature Optimum
61	H30	Moderate	65°
72	V66	Similar to wild type	70°
81	P128	Low	Not tested
92	I158	Low	Not tested
3	G125	Similar to wild type	Not tested
13/14	K201	low	65°

Pyrococcus furiosus gene for archaeal histone (Hmf-like) (Fig. 17-A)
(ACCESSION No: AB013081)

```
M M G E L P I A P V D R L I R K A G 18
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
A Q R V S E Q A A K V L A E H L E E 36
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
K A I E I A K K A V D L A K H A G R 54
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
K T V K V E D I K L A I K S * 69
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA 207
```

(Hmf-like)-Taq DNA polymerase fusion protein (Fig. 17-B)

```
M M G E L P I A P V D R L I R K A G 18
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
A Q R V S E Q A A K V L A E H L E E 36
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
K A I E I A K K A V D L A K H A G R 54
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
K T V K V E D I K L A I K S 69
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC
```

G G G
// GGC GGC GGT

```
V T S G M L P L F E P K G R V L L V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG
D G H H L A Y R T F H A L K G L T T
```

36/186

Fig. 17B (cont)

GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC
 S R G E P V Q A X Y G F A K S L L K
 AGC CGG GGG GAG CCG GTG CAG GCC CTC TAC GGC TTC GCC AAG AGC CTC CTC AAG
 A L K E D G D A V I V F D A K A P
 GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC
 S F R H E A Y G G Y K A G R A P T P
 TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACC CCA
 E D F P R Q L A L I K E L V D L L G
 GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG
 L A R L E V P G Y E A D D V L A S L
 CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG
 A K K A E K E G Y E V R I L T A D K
 GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CCG ATC CTC ACC GCC GAC AAA
 D L Y Q L L S D R I H V L H P E G Y
 GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC
 L I T P A W L W E K Y G L R P D Q W
 CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG
 A D Y R A L T G D E S D N L P G V K
 GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG
 G I G E K T A R K L L E E W G S L E
 GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA
 A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CCG CTG AAG CCC GCC ATC CCG GAG AAG ATC CTG
 A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

Fig. 17B (cont)

L P L E V D F A K R R E P D R E R L
 CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
 L E S P K A L E E A P W P P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC
 F V G F V L S R K E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
 L A A A R G G R V H R A P E P Y K A
 CTG GCC GCC GCC AGG GGG GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
 L R D L K E A R G L L A K D L S V L
 CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
 A L R E G L G L P P G D D P M L L A
 GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
 Y L L D P S N T T P E G V A R R Y G
 TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG TAC GGC
 G E W T E E A G E R A A L S E R L F
 GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC
 A N L W G R L E G E E R L L W L Y R
 GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG AGG CTC CTT TGG CTT TAC CGG
 E V E R P L S A V L A H M E A T G V
 GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG
 R L D V A Y L R A L S L E V A E E I
 CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
 A R L E A E V F R L A G H P F N L N
 GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

Fig. 17B (cont)

S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC
 G K T E K T G K R S T S A A V L E A
 GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTC GAG GCC
 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC
 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG
 G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC ACG GGC AGG CTA AGT
 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG
 I R R A F I A E E G W L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT
 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC
 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC
 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC GGC AAG ACC ATC
 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC
 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC
 K V R A W I E K T L E E G R R R G Y

AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC
 V E T L F G R R Y V P D L E A R V
 GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
 K S V R E A A E R M A F N M P V Q G
 AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
 T A A D L M K L A M V K L F P R L E
 ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
 E M G A R M L L Q V H D E L V L E A
 GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
 P K E R A A E A V A R L A K E V M E G
 CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG
 V Y P L A V P L E V E V G I G E D W
 GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG
 L S A K E G I D G R G G G H H H
 CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGC CAT CAT CAT
 H H *
 CAT CAT TAA

Tag DNA polymerase-(HMF-like) fusion protein (Fig. 17-C)

G G G
 // GGC GGC GGT

V T S G M L P L F E P K G R V L L V
 GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG
 D G H H L A Y R T F H A L K G L T T

Fig 17c (cont)

GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC
 S R G E P V Q A X Y G F A K S L L K
 AGC CGG GGG GAG CCG GTG CAG GCG CTC TAC GGC TTC GCC AAG AGC CTC CTC AAG
 A L K E D G D A V I V V F D A K A P
 GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC
 S F R R H E A Y G G Y K A G R A P T P
 TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGC GCC ACC CCA
 E D F P R Q L A L I K E L V D L L G
 GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG
 L A R L E V P G Y E A D D V L A S L
 CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG
 A K K A E K E G Y E V R I L T A D K
 GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA
 D L Y Q L L S D R I H V L H P E G Y
 GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC
 L I T P A W L W E K Y G L R P D Q W
 CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AAG CCC GAC CAG TGG
 A D Y R A L T G D E S D N L P G V K
 GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG
 G I G E K T A R K L L E E W G S L E
 GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA
 A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG
 A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

Fig 17C (cont)

L P L E V D F A K R R E P D R E R L
 CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
 L E S P K A L E E A P W P P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG CCG GAA GGG GCC
 F V G F V L S R K E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
 L A A A R G G R V H R A P E P Y K A
 CTG GCC GCC GCC AGG GGG GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
 L R D L K E A R G L L A K D L S V L
 CTC AGG GAC CTG AAG GAG GCG CGG GGC CTT CTC GCC AAA GAC CTG AGC GTT CTG
 A L R E G L G L P P G D D P M L L A
 GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
 Y L L D P S N T T P E G V A R R Y G
 TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
 G E W T E E A G E R A A L S E R L F
 GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC
 A N L W G R L E G E E R L L W L Y R
 GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG AGG CTC CTT TGG CTT TAC CGG
 E V E R P L S A V L A H M E A T G V
 GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG
 R L D V A Y L R A L S L E V A E E I
 CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
 A R L E A E V F R L A G H P F N L N
 GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

Fig 17C (cont)

S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC
 G K T E K T G K R S T S A A V L E A
 GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTG GAG GCC
 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC
 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG
 G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC ACG GGC AGG CTA AGT
 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG
 I R R A F I A E E G W L L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT
 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC
 R V F Q E E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC
 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GGC GCC AAG ACC ATC
 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC
 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC
 K V R A W I E K T L E E G R R R G Y

Fig. 17C (cont)

AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC
V E T L F G R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
K S V R E A A E R M A F N M P V Q G
AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
T A A D L M K L A M V K L F P R L E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
P K E R A³ E A V A R L A K E V M E G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG
V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG
L S A K E G I D G R G G G G H H H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGG CAT CAT CAT
H H //
CAT CAT //
M M G E L P I A P V D R L I R K A G 18
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
A Q R V S E Q A A K V L A E H L E E 36
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
K A I E I A K K A V D L A K H A G R 54
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
K T V K V E D I K L A I K S * 69
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Pfu DNA Polymerase (WT) -(HMF-like) fusion protein (Fig. 17-D)

//

ccctggtcct ggggccacat atatgttctt actgccttt atgaagaatc ccccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaag ttatttctat
caactctaca cctccccctat ttctctctt atgagattt taagtatagt tatagagaag
gttttatact ccaactgag ttagtagata tgtggggagc ataatgatt tagatgtgga
ttacataact gaagaaaggaa aacctgttat taggtattc aaaaaagaga acggaaaatt
taagatagag catgatagaa ctttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaagggcat ggaagatgtg tgagaattgt
tgatgtagag aaggttgaga aaaagtctt cggcaagcct attaccgtgt ggaacttta
tttggaacat cccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt
tgtggacatc ttcgaatagc atattccatt tgcgaagaga taccatcag acaaggcct
aataccaatg gaagggggaag aagagctaaa gattcttgcc ttcgatatag aaacctcta
tcacgaaagg gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaaagcaag gtgattactt ggaanaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaact
tgggatataa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag

Fig. 17D (cont)

gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttgaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagccctgg gaaagtggag agaacccttga
gaaggttgcc aaatactcga tggaaagtgc aaaaggcaact tatgaactcg ggaagaat
cctccaatg gaaattcagc ttccaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaacctg tagagtgtt ctacttagg aaagccctacg aaagaaaacga
agtagctcca aacaagccaa gtgaagaggga gtatcaaaaga aggtctcaggg agagctacac
aggtggatc gttaaagagc cagaaaaaggg gttgtggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccaaatgtt tctcccgata ctctaatct
tgagggatgc aagaactatg atatcgctcc tcaagtatgc cacagtctt gcaaggacat
ccctggttt ataccaagtc tcttggaca ttgttagag gaaagacaaa agatthaagac
aaaaatgaaag gaaactcaag atccctataga aaaaatactc cttagctata gacaaaaaagc
gataaaactc ttagcaaat cttctacgg atatlatgc tatgcaaaag caagatgtta
ctgtaaggag tgtgtcgaag gcgttactgc ctggggaaaga aagtacatcg agttaagtatg
gaaggagctc gaagaaaagt ttgatttaa agtcctctac attgacactg atgtctcta
tgcaactatc ccaggaggag aaagtggagg aataaagaaa aaggctctag aattgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaaggaa aagtcattac
tcgtgttta gagatagtta ggaagagtg gagtgaat t gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga

Fig 17D (cont)

agtaatacaa aagcttgcca attatgaat tccaccagag aagctcgcaa tatatgagca
gataaccaaga ccattacatg agtataagc gatagtcct cactagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatgta attgataca tagtacttag
aggcgatggt ccaatlagca atagggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagatatc acattgagaa ccaggttctt ccagcggtag ttaggatatc
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacattt aaaaatcccta gaaaagcgat agatatcaac tttattctt
tctaaccctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttattta
tgggtaatta aaaaccatg ctctgggag aatcttcgaa taaatccct aacttcagc
tttgctaagt gaatagaata aacaacatca ctcaattcaa accgcttcgt tagaatggt
ctatctgcat gcttctctgg ctcggaanng gaggatcct aacaacagta tcaacattct
cagagaattg agaaacatca gaaacttga ctctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggc tcctcgtcaa ttgcgagac gtagatcttt
tttgctccaa gcagagccgc tccaatggt aacacccctg ttcccgacc cagtccgct
acaattttt cctgtatct cctaagtat aagcaagcca aaggagagta gatgctacct
ttccgggagt ttgtattgc tctagccaag gtttggatt ttgaaacct ttaactctgg
aaagtataat ttcaagctcc ttctcttca tgacagatga aaaattgttt tgtctcttt
taactttac agaaataact gtctcaatt atgacaactc ttgacatttt tacttcatta
ccagggtaat gttttaagt atgaatttt tcttcatag aggaggnnn ngtcctctc

47186

ctcgatttcc ttggttgtc tccatatgat aagcttccaa agtgggtgtt cagacttta
gacactcaaa taccagacga caatggtgtg ctcaactcaag ccccatatgg gtlgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntccnga
aagattgaga tgttcttg //

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

(HMF-like) - Pfu DNA Polymerase (WT) fusion protein (Fig. 17-E)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

ccctggtcct gggccacat atatgttctt actgccttt atgaagaatc ccccgctgc
tctaacctgg gttatagtga caaatcttcc tccaccacgg cccaagaagg ttatttctat
caactctaca cctccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttactt ccaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggtattc aaaaagaga acggaaaatt
taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaagggcat ggaagatttg tgagaattgt

Fig 17E (cont)

tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaacttta
tttgaaacat cccaagatg tccccactat tagagaaaaa gtagagaac atccagcagt
tgtggacatc ttcgaatacg atatccatt tgcagaagaga taccatcgc acaaggcct
aataccaatg gagggggaag aagagctaaa gattctgcc ttcgatatag aaaccctcta
tcacgaagga gaagagtttg gaaaagccc aattataatg attagttatg cagatgaaaa
tgaagcaaaag gtgattactt ggaaaaacat agatcctcca tacgttgagg ttgtatcaag
cgaagagagag atgataaaga gatttctcag gattatcagg gagaagatc ctgacattat
agttaactat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaact
tgggatlaaa ttaaccattg gaagagatgy aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggagaatat acatttcgac ttgtatcatg taataacaag
gacaataaat ctccccaacat acacactaga ggctgtatat gaagcaattt ttggaagccc
aaaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaacctga
gagagttgcc aaatactcga tggagaatgc aaagccaact tatgaactcg ggaagaaltt
cctccaatg gaaatlcagc ttccaagatt agttggacaa cctttatgg atgtttcaag
gtcaagcaca gggaaacctg tagagtgtt cttaactag aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaaagaga gtatcaaga aggcacaggg agagctacac
aggtggttc gttaagagc cagaaaaagg gtgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctccgata cttaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaagacat

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Fig. 17E (cont)

ccctggtttt ataccgaagtc tcttgggaca ttgttagag gaaagaccaa agattaaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc ctlgactata gacaaaaagc
gataaaactc ttagcaaat cttctacgg atattatggc tatgcaaaag caagatgta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaaga aagtacatcg agttaagtatg
gaaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atgtctcta
tgcaacctatc ccaaggaggag aaagtgaaga aataaagaaa aaggctctag aattgtaaa
atacataaat tcaaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaaggaa aagtcattac
tcgtggttta gagatagtta ggaagagattg gagtgaaat gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaaaga gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggtcct cagctagctg ttgcaaaaga
actagctgct aaaggagtta aaataaagcc aggaatgta attggataca tagtacttag
aggcgatggt ccaattagca ataggccaat tctaactgag gaatacgatc ccaaaaagca
caagtatgac gcagaatat acattgagaa ccaggttctt ccagcggtac ttagatat
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatla aaaaatccta gaaaagcgat agatatcaac tttattctt
tctaaccctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tggttaatta aaaaccatg ctcttggag aatcttcgaa taaatccct aacttcaggc

ttgctaagt gaatagaata aacaacatca ctcaattcaa acgccttcgt tagaatggt
 ctatctgcat gcttctctg ctcggaanng gaggttcat aacaacagta tcaacattct
 cagaagaattg agaaacatca gaaacttga ctctacaac atttctaact ttgcaactct
 tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa ttgcgacgac gtagatcttt
 ttgctcccaa gcagagccgc tccaatgat aacacccctg ttcccgacc caagtccgct
 acaattttt ccttgatct cctaattgat aagcaagcca aaggagagta gatgctacct
 ttccgggagc ttgtatgac tctagccaag gtttggaatt ttgaatcct ttaactctg
 aaagtataat ttcaagctcc tcttcttca tgacagatga aaaattgtt tgtctcttt
 taactttac agaataact gtctcaatt atgacaactc ttgacatttt tacttcatta
 ccagggtaat gtttttaagt atgaatttt tcttcataag aggaggnnn ngtcctctc
 ctcgatttcc ttggtgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta
 gacactcaaa taccagacga caatgtgtg ctcaactcaag ccccatatgg gttgagaaaa
 gtagaagcgg cactactcag atgctcccc aggaatgagg ttgtgtagc tcntccnga
 aagattgaga tgttcttg // TGA

(HMF-like) - PFU DNA POLYMERASE (V93 R OR E) fusion protein (Fig. 17-F)

Fig 17 F (cont)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATTTTATG ATGTGATTA CATACTGAA GAAGGAAAC CTGTTATTAG GCTATTCAA 60 AAAGAGAAGC GAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTACGCT 120 CTCTCAGGG ATGATTCAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGCATGGA 180
AAGATTGTGA GAATGTGTA TGTAGAGAAG GTTGAGAAA AGTTCTCGG CAAGCCTATT 240 ACCGTGTGA AACTTTATTT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAGAT TCTTGCCCTC 420 GATATAGAAA CCTCTATCA CGAAGAGAA
GAGTTTGAA AAGGCCAAT TATAATGATT 480 AGTTATGAG ATGAATGCA AGCAAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTTCC ATATTAGCG 660 AAAAGGCGAG AAAAAGCTTG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGCGATAT GACGCTGTA GAAGTCAAG GAAGATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTG GAAAGCCAAA GGAGAAGTA TACGCCGACG AGATAGCAAA AGCCTGGAA 900
AGTGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCACTTAT 960 GAACTCGGGA AAGAATTCTT TCCAATGAA
ATTGAGCTTT CAAGATTAGT TGGACAACTT 1020 TTATGGATG TTCAAGGTC AAGCACAGGG AACCTGTAG AGTGTCTT ACTTAGAAA
1080 GCCTACGAA GAAACGAAGT AGCTCCAAC AAGCCAAGTG AAGAGAGTA TCAAGAAGG 1140 CTCAGGAGA GCTACACAGG
TGGAATCGTT AAAGAGCCAG AAAAGGGTT GTGGAAAAC 1200 ATAGTATACC TAGATTTAG AGCCCTATAT CCTCGATTA TAATTACCA
CAATGTTTCT 1260 CCCGATCTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGA
AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC
CTATAGAAA AATACTCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGTAAGT TAAGGAGTGT GCTGAGAGCG TTAAGTCTG GGAAGAAAG 1560 TACATCGAGT TAGTATGAA GGAGCTCGAA
GAAAAGTTG GATTAAAGT CCTTACATT 1620 GACACTGATG GTCTTATGC AACTATCCA GGAGAGAAA GTGAGGAAAT AAAGAAAAAG
1680 GCTCTAGAA TTTAAATA CATAAATTCA AAGCTCCTG GACTGCTAGA GCTGAATAT 1740 GAAGGTTT ATAAGAGGG
ATTCTTCGTT ACGAAGAGA GGTATGAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGAG
TGAATTTGCA 1860 AAAGAACTC AAGCTAGAGT TTTGAGACA ATACTAAAC ACGGAGATGT TGAAGAGCT 1920 GTGAGATAG
TAAAGAGAGT AATACAAAAG CTGCAATT ATGAATTTCC ACCAGAGAAG 1980 CTGCAATAT ATGAGCAGAT AACAGAGCA TTACATGAGT
ATAAGCGAT AGTCTCAC 2040 GTAGCTGTG CAAAGAACT AGCTGCTAA GGAGTTAAA TAAAGCCAGG AATGTAATT 2100
GGATACATAG TACTTAGAG CGATGTCCA ATTAGCAATA GGCAATTCT AGCTGAGGAA 2160 TACGATCCA AAAGCACAA GTATAGCGA
GAATATTACA TGGAGAACCA GGTCTTCCA 2220 GCGTACTTA GATATTGGA GGAATTGGA TACAGAAAG AAGACCTCAG ATACCAAAAG
2280 ACAAGACAAG TCGGCTAAC TTCTGCTT AACATTAAA AATCC //

// TGA

PFU DNA POLYMERASE (V93 R OR E) - (HIMf-like) fusion protein (Fig. 17-G)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGATTTA CATACTGAA GAAGGAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGACG GAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATTA CATTACGCT 120 CTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGCATGGA 180
AAGATTGTGA GAATTGTGA TGTAAGAGAG GTTGAGAAA AGTTCTCCG CAAGCCTATT 240 ACCGTGTGA AACTTTATT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAG AGCTAAGAT TCTTGCCCTTC 420 GATATAGAAA CCTCTATCA CGAAGGAGAA
GAGTTTGAA AAGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAATAATGA AGCAAGGTG ATTACTTGA AAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATCCC ATATTAGCG 660 AAAAGGGCAG AAAAAGCTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTG GAAAGCCAAA GGAGAAGTA TACGCCGACG AGATAGCAAA AGCCTGGAA 900
AGTGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCCAA GGCACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGAA
ATTGAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGAGT TTCAAGGTC AAGCACAGGG AACCTGTAG AGTGTTCTT ACTTAGGAA
1080 GCCTAGGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGAGTA TCAAGAGAG 1140 CTCAGGAGA GCTACACAGG
TGGAATCGTT AAAGAGCCAG AAAAGGGTT GTGGGAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCA
CAATGTTTCT 1260 CCCGATCTC TAAATCTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGA
AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGA 1380 AGACAAAGA TTAAGACAAA AATGAAGGA ACTCAAGATC
CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAATTTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGTTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGAAGAAAG 1560 TACATCGAGT TAGTATGAA GAGCTCGAA
GAAAAGTTTG GATTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAT AAAGAAAAAG
1680 GCTCTAGAAT TTGTAAATA CATAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAAGGTTT ATAAGAGGGG
ATTCTTCGTT ACGAAGAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGAG
TGAATTTGCA 1860 AAAGAACTC AAGCTAGAGT TTGAGAGACA ATACTAAAC ACGAGATGT TGAAGAAGCT 1920 GTGAGATAG
TAAAGAGAGT AATACAAAAG CTTCGCAATT ATGAAATCC ACCAGAGAG 1980 CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT
ATAAGCGGAT AGTCCCTCAC 2040 GTAGCTGTG CAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGTAATT 2100
GGATACATAG TACTTAGAGG CGATGTTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA
GAATATTACA TGGAGAACCA GTTCTTCCA 2220 GCGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG
2280 ACAAGACAAG TCGCCTAAC TTCCTGGCTT AACATTAAA AATCC // 2328

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162

53/18

AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

PFU DNA POLYMERASE (G387P/V93R OR E) -(HMF-like) fusion protein (Fig. 17-H)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGATTTA CATACTGAA GAAGGAAAC CTGTTATTAG GCTATTCAA 60 AAAGAGAACG GAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTACGCT 120 CTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGG AAGGCATGGA 180
AAGATTGTGA GAATTGTGA TGTAGAGAAG GTTGAGAAA AGTTCTCGG CAAGCCTATT 240 ACCGTGTGA AACTTTATT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGCCTAAT ACCAATGAG GGGAGAAG AGCTAAGAT TCTTGCCCTC 420 GATATAGAAA CCTCTATCA CGAAGGAGAA
GAGTTTGAA AAGCCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAATGA AGCAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATCCC ATATTAGCG 660 AAAAGGCGAG AAAAAGCTGG GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGCGATAT GACGCTGTA GAAGTCAAG GAAGATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAA AGCCTGGGAA 900
AGTGAGAGA ACCTGAGAG AGTGGCCAAA TACTCGATGG AAGATGCAA GCGAATTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGA
ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGATG TTTCAGGTC AAGCACAGGG AACCTGTAG AGTGTTCTT ACTTAGGAAA
1080 GCCTACGAAA GAAAGAAAGT AGCTCCAAC AAGCCAAGTG AAGAGAGTA TCAAGAAAG 1140 CTCAGGAGA GCTACACACC
NGGATTCGTT AAAGAGCCAG AAAAGGGGT GTGGAAAAC 1200 ATAGTATACC TAGATTTAG AGCCCTATAT CCCTCGATTA TAATTACCA
CAATGTTTCT 1260 CCCGATCTC TAAATCTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTCTGCA
AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGA ACTCAAGATC
CTATAGAAA AATACTCCT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAATTCTT TCTACGATA TTATGGCTAT 1500
GCAAAAGCAA GATGTTACTG TAAGAGTGT GCTGAGAGCG TTAAGGAAAG 1560 TACATCGAGT TAGTATGGA GAGCTCGAA
GAAAAGTTG GATTAAAGT CCTTACATT 1620 GACACTGATG GTCTTATGC AACTATCCA GGAGGAGAA GTGAGGAAAT AAAGAAAAG
1680 GCTCTAGAAAT TTGTAAATA CATAAATCA AAGCTCCCTG GACTGCTAGA GCTGAATAT 1740 GAAGGTTTT ATAAGAGGG
ATTCTTCGTT ACGAAGAGA GGTATGCAAT AATAGATGA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGA GAGATTGGAG
TGAATTTGCA 1860 AAAGAACTC AAGCTAGAGT TTGGAGACA ATACTAAAC ACGAGAGTGT TGAAGAAGCT 1920 GTGAGATAG
TAAAGAAAGT AATACAAAAG CTGCAATAT ATGAATTC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT
ATAAGCGAT AGTCTCTAC 2040 GTAGCTGTG CAAAGAACT AGCTGCTAA GGAGTTAAA TAAAGCCAGG AATGTAATT 2100
GGATACATAG TACTTAGAGG CGATGTCCA ATTAGCAATA GGGCAATCT AGCTGAGGA 2160 TACGATCCA AAAAGCACAA GTATGACGA
GAATATTACA TGGAGAACA GTTCTTCCA 2220 GCGTACTTA GGATATTGA GGAGTTTGA TACAGAAAGG AAGACCTCAG ATACCAAAAG
2280 ACAAGACAAG TCGGCTTAC TTCCTGGCTT AACATTAAA AATCC //

2328

28155


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//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT      54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA      108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA      162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

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(HMF-like) - PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein (Fig. 17-1)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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ATG ATG GGA GAA TTA CGA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT      54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA      108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA      162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

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//ATGATTAG ATGTGATTA CATACTGAA GAAGGAAAC CTGTTATTAG GCTATTCAA 60 AAAGAGAACG GAAATTAA GATAGACAT
GATAGAACTT TTAGACCATTA CATTACGCT 120 CTCTCAGGG ATGATTCAA GATTGAAGAA GTTAGAATAA TAACGGGGA AAGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCG CAAGCCTATT 240 ACCGTGTGA AACTTTATT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGACATC CAGCAGTTGT GGACATCTC GAATACGATA TTCCATTTC AAAGAGATAC 360
CTCATCGACA AAGCCCTAAT ACCAATGAG GGGGAGAAG AGCTAAGAT TCTTGCCCTC 420 GATATAGAAA CCCTCTATCA CGAAGAGAA
GAGTTTGAA AAGGCCCAAT TATAATGATT 480 AGTTATGAG ATGAATATGA AGCAAGGTG ATTACTTGA AAAACATAGA TCTTCCATTAC 540
GTTGAGGTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGAG 600 AAGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATCCC ATATTAGCG 660 AAAGGGCAG AAAAAGCTTG GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGCTGTA GAAGTCAAG GAAGATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC ATAATCTC
CCACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGAGAGA ACCTTGAGAG AGTGGCCAAA TACTCGATG AAGATGCAAA GGCACTTAT 960 GAACTCGGA AAGATTCTT TCCAATGAA
ATTGAGCTTT CAAGATTAGT TGGACAACT 1020 TTATGGAGT TTCAAGGTC AAGCACAGG AACCTGTAG AGTGTTCTT ACTTAGGAAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAC AAGCCAAGT AAGAGAGTA TCAAGAAGG 1140 CTCAGGAGA GCTACACACC
NGGATTCGTT AAAGAGCCAG AAAAGGGTT GTGGAAAAC 1200 ATAGTATACC TAGATTTAG AGCCCTATAT CCCTCGATTA TAATTACCA
CAATGTTCT 1260 CCCGATCTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGA
AGGACATCCC TGGTTTATA CCAAGTCTCT TGGACATTT GTTAGAGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC
CTATAGAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAATTTCT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGTTACTG TAAGAGTGT GCTGAGAGCG TTACTGCCCTG GGGAAGAAAG 1560 TACATCGAGT TAGTATGAA GGAGCTCGAA
GAAAAGTTTG GATTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCA GGAGAGAGAA GTGAGGAAT AAAGAAAAG

```

1680 GCTCTAGAAT TTGTAATAA CATAAATCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGTTT ATAAGAGGG
 ATTCTCGT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTAGAG ATAGTTAGGA GAGATTGGAG
 TGAATTGCA 1860 AAAGAACTC AAGCTAGAGT TTGGAGACA ATACTAAAC ACGAGATGT TGAAGAACT 1920 GTGAGAATAG
 TAAAGAAGT AATACAAAAG CTGCCAAT ATGAATTCC ACCAGAGAAG 1980 CTCGCAATAT ATGACAGAT AACAGAACA TTACATGAGT
 ATAGCGGAT AGTCCCTAC 2040 GTAGCTGTG CAAAGAACT AGCTGCTAA GGAGTTAAA TAAAGCCAGG AATGTAATT 2100
 GGATACATAG TACTTAGAG CGATGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGAA 2160 TACGATCCA AAAAGCACAA GTATGACGA
 GAATATTACA TGGAGAACA GGTCTTCCA 2220 GCGTACTTA GATATTGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG
 2280 ACAAGACAAG TCGCCTAAC TTCCTGGCTT AACATTAAA AATCC //TAG 2328

(HMF-LIKE) -PFU DNA POLYMERASE (D141A/E143A/V93R OR E) fusion protein
(Fig. 17-J)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
 AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
 AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATTTAG ATGTGATTA CATACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60 AAAGAGAAG GAAATTAA GATAGACAT
 GATAGAACTT TTAGACCATA CATTACGCT 120 CTCTCAGGG ATGATTCAA GATTGAAGAA GTTAAGAAA TAACGGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTGA TGTAGAGAAG GTTGAGAAA AGTTCTCGG CAAGCCTATT 240 ACCGTGTGA AACTTTATT GGAACATCCC
 CAAGATXXX CCACATATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTGCG AAAGAGATAC 360
 CTCATCGACA AAGCCTAAT ACCAATGAG GGGAGAAG AGCTAAGAT TCTTGCTTC 420 GCNATAGCNA CCTCTATCA CGAAGAGAA
 GAGTTTGAA AAGCCCAAT TATAATGATT 480 AGTTATGAG ATGAATAATGA AGCAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
 GTTGAGGTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGAG 600 AAGGATCTG ACATTATAGT TACTTATAT
 GGAGACTCAT TCGCATTCCC ATATTAGCG 660 AAAAGGCGAG AAAAAGCTTG GATTAAATTA ACCATTGGA GAGATGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGCGATAT GACGCTGTA GAAGTCAAG GAAGATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
 CCAACATACA CACTAGAGG TGTATATGAA 840 GCAATTTTG GAAAGCCAAA GGAGAAGTA TACGCCGACG AGATAGCAA AGCCTGGGA 900
 AGTGAGAGA ACCTTGAGAG AGTTGCCAAA TACTGATGG AAGATGCAA GGCACCTAT 960 GAACTCGGA AAGAATTCCT TCCAATGAA
 ATTCACTTT CAAGATTAGT TGGACAACCT 1020 TTATGGATG TTCAAGTTC AAGCACAGG AACCTTGTAG AGTGTCTT ACTTAGGAAA
 1080 GCCTACGAAA GAAACGAAGT AGCTCCAAC AAGCCAAGT AAGAGAGTA TCAAGAAGG 1140 CTCAGGAGA
 GCTACACAGG.TGGATTCGTT AAAGAGCCAG AAAAGGGTT GTGGAAAAC 1200 ATAGTATACC TAGATTTTAT AGCCCTATAT CCCTGATTA
 TAATTACCA CAATGTTTCT 1260 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGCCAC 1320

AAGTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380 AGACAAAGA TTAAGACAA AATGAGGAA
 ACTCAAGATC CTATAGAANA AATACTCCTT 1440 GACTATAGAC AAAAGCGAT AAAACTCTTA GCAATTCTT TCTACGATA TTATGCTAT
 1500 GCAAAAGCAA GATGTAAGT TAAAGAGTGT GCTGAGAGCG TTAAGAGCGG GGAAGAAAG 1560 TACATGAGT TAGTATGAA
 GGAGCTCGAA GAAAGTTTG GATTAAAGT CCTCTACAT 1620 GACACTGATG GTCTTATGC AACTATCCCA GGAGAGGAA GTGAGGAAT
 AAAGAAAAG 1680 GCTCTAGAAT TTGTAATAA CATAAATCA AAGCTCCCTG GACTGCTAGA GCTGAATAT 1740 GAAGGTTTT
 ATAGAGGGG ATTCTTCGT ACGAAGAAGA GTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTAGAG ATAGTTAGGA
 GAGATTGAG TGAATTGCA 1860 AAAGAACTC AAGCTAGAGT TTGGAGACA ATACTAAAC ACGAGATGT TGAAGAAGCT 1920
 GTGAGATAG TAAAGAAAGT AATACAAAAG CTGCAATT ATGAATTC ACCAGAGAAG 1980 CTGCAATAT ATGAGCAGAT AACAGACCA
 TTACATGAGT ATAGGCGAT AGTCTCTAC 2040 GTAGCTGTG CAAGAAACT AGCTGCTAA GAGTTAAA TAAAGCCAG AATGGTAATT
 2100 GGATACATAG TACTTAGAG CGATGTCCA ATTAGCAATA GGCATTTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACA
 GTATGACGCA GAATATTACA TGGAGAACCA GTTCTTCCA 2220 GCGTACTTA GGATATTGA GGGATTGGA TACAGAAAGG AAGACCTCAG
 ATACCAAAG 2280 ACAAGACAAG TCGGCTTAC TTCCTGGCTT AACATTAAA AATCC // 2328

TGA

PFU DNA POLYMERASE (D141A/E143A/V93R OR E) - (HMF-LIKE) fusion protein
 (Fig. 17-K)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
 V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTATG ATGTGATTA CATACTGAA GAAGGAAAC CTGTATTAG GCTATTCAA 60 AAAGAGACG GAAATTTAA GATAGAGCAT
 GATAGAACTT TTAGACCATA CATTACGCT 120 CTCTCAGG ATGATTCAA GATTGAAGA GTTAAGAAA TAACGGGGA AAGCATGGA 180
 AAGATTGTGA GAATTGTGA TGTAGAGAA GTTGAGAAA AGTTTCTCG CAAGCCTATT 240 ACCGTGTGA AACTTTATT GGAACATCCC
 CAAGATXXX CCACTATTAG AGAAAAGTT 300 AGAGACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
 CTCATCGACA AAGGCTTAAT ACCAATGGAG GGGAGAGAAG AGCTAAGAT TCTGCTTC 420 GCNATAGCNA CCTCTATCA CGAAGAGAA
 GAGTTTGAA AAGGCCAAT TATAATGAT 480 AGTTATGAG ATGAATAATGA AGCAAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
 GTTGAAGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGAG 600 AAGATCCTG ACATTATAGT TACTTATAT
 GGAGACTCAT TCGCATTCCT ATATTAGCG 660 AAAAGGGCAG AAAAAGCTTG GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGCGATAT GACGCTGTA GAAGTCAAG GAAGATACA TTTCAGCTG 780 TATCATGTAA TAACAAGGAC AATAATCTC
 CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGAA 900
 AGTGAGAGA ACCTTGAGAG AGTGCCAAA TACTCGATGG AAGATGCAA GCAACTTAT 960 GAAGTGGGA AAGAAATTCCT TCCAATGAA
 ATTACGCTT CAAGATTAGT TGGACAACCT 1020 TTATGGAGT TTCAAGGTC AAGCAGAGG AACCTTGTAG AGTGTTCTT ACTTAGAAA
 1080 GCCTACGAAA GAAAGGAAGT AGCTCCAAC AAGCCAAGT AAGAGGAGTA TCAAGAGAG 1140 CTCAGGAGA
 GCTACACAGG.TGATTCGTT AAAGAGCCAG AAAGGGGT GTGGAAAAC 1200 ATAGTATACC TAGATTTAG AGCCCTATAT CCCTCGATTA
 TAATTACCA CAATGTTCT 1260 CCCGATCTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCTCA AGTAGCCAC 1320

AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA
 ACTCAAGATC CTATAGAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAACCTCTTA GCAAATCTT TCTACGGATA TTATGGCTAT
 1500 GCAAAAGCAA GATGTAAGT TAAGAGTGT GCTGAGAGCG TTAAGAGCGG GGAAGAAG 1560 TACATCGAGT TAGTATGAA
 GGAGCTCGAA GAAAGTTTG GATTAAAGT CCTTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGAGGAAA GTGAGGAAAT
 AAAGAAAAG 1680 GCTCTAGAAT TTGTAATAA CATAAATTC AAGCTCCCTG GACTGCTAGA GCTGAATAT 1740 GAAGGTTT
 ATAAGAGGGG ATTCTTCGTT ACGAAGAGA GGTATGAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTAGAG ATAGTTAGGA
 GAGATTGAG TGAATTGCA 1860 AAAGAACTC AAGCTAGAGT TTGAGAGCA ATACTAAAC ACGAGATGT TGAAGAAGCT 1920
 GTGAGAATAG TAAAGAAGT AATACAAAAG CTGCAATT ATGAAATCC ACCAGAGAAG 1980 CTCGAATAT ATGAGCAGAT AACAAGACCA
 TTACATGAGT ATAAGCGAT AGGTCTCAC 2040 GTAGCTGTTG CAAAGAACT AGCTGCTAAA GAGTTAAA TAAAGCAGG AATGTTAAT
 2100 GGATACATAG TACTTAGAG CGATGTCCA ATTAGCAATA GGGCAATCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA
 GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220 GCGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG
 ATACCAAAAG 2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAA AATCC // 2328

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
 AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
 AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

KOD DNA POLYMERASE - (HIMf-like) fusion protein (Fig. 17-1)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCCTCG ACACCTGACTA CATAACCGAG GATGGAAGC CTGTCAATAG AATTTCAG 60
 AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCTTA CTCTACGCC 120
 CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
 ACGTTGTAA CGGTTAAGCG GGTGAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAATT 240
 GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
 CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
 CTCATAGACA AGGGAATTAGT GCCAATGAA GCGGACGAGG AGCTGAAAT GCTCGCCTTC 420
 GACATTGAAA CTCTCTACCA TGAGGGCCGAG GAGTTCGCCG AGGGCCAAT CCTTATGATA 480
 AGCTACGCCG ACGAGGAAGG GGGCAGGGTG ATAAGTTGGA AGAAGCTGGA TCTCCCTAC 540
 GTTGACGTCG TCTGACGGA GAGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
 AAAGACCCGG ACGTTCTCAT AACCTACAAC GCGGACAAC TCGACTTCGC CTATCTGAAA 660
 AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
 ATTCAGAGGA TGGCGACAG GTTTCCCGTC GAAGTGAAG GACGATACA CTTCGATCTC 780
 TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840

GCCGCTCTCC GTCAGCCGAA GGAGAAGTT TACGCTGAGG AAATAACCAAC AGCCTGGGAA 900
 ACCGGCGAGA ACCTTGAGAG AGTCGCCCCG TACTCGATGG AAGATGCGAA GGTACATAC 960
 GAGCTTGGGA AGGAGTTCCT TCCGATGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
 CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
 GCCTATGAGA GGAATGAGCT GGGCCCGAAC AAGCCCGATG AAAAGAGCT GGCAGGAAGA 1140
 CGGCAGAGCT ATGAAGGAGG CTATGTAATA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
 GTGTACCTAG ATTTAGATC CCTGTACCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
 GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGAGT CGGCCACCGC 1320
 TTCTGCAAGG ACTTCCGAGG ATTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
 CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
 TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
 AGGCGCGCT GGTACTGCAA GGAGTGTGA GAGAGCGTAA CGGCCTGGGG AAGGAGTAC 1560
 ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
 ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
 ATGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGCGG CGCTTGAGCT CGAGTACGAG 1740
 GGCTTCTACA AACGCGGCTT CTTGCTCAGG AAGAAGAAAT ATGCGGTGAT AGACGAGGAA 1800
 GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGCGCTG ACTGAGCGA GATAGCGAAA 1860
 GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAGGACG GTGACGTCGA GAAGCCGCTG 1920
 AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
 GTGATCCACG AGCAGATAAC GAGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
 GCCGTTGCCA AGAGGTTGCC CGCGAGAGGA GTCAAATAAC GCCCTGGAAC GGTGATAAGC 2100
 TACATCGTGC TCAAGGCTC TGGGAGGATA GCGGACAGGG CGATACCCTT CGACGAGTTC 2160
 GACCCGACGA AGCACAAAGTA CGACGCCGAG TACTACATTG AGAACCAAGT TCTCCAGCC 2220
 GTTGAGAGAA TTCTGAGAGC CTTGGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAAGACG 2280
 AGACAGGTTG GTTGAGTGC TTGGCTGAAG CCGAAGGGA CT 2325
 //ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA AGA CTT ATA AGA AAG GCT GGT 54
 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
 AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
 AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

(HMF-like) - KOD DNA POLYMERASE fusion protein (Fig. 17-M)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54

Fig 17M (cont)

GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
 AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
 AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATCCTCG ACACTGACTA CATAACCGAG GATGAAAGC CTGTCATAAG AATTTCAAG 60
 AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCTTA CTCTACGCC 120
 CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGCACC GG 180
 ACGGTTGTAA CGGTTAAGCG GGTGAAAG GTTCAGAAGA AGTTCTCGG GAGACCAGTT 240
 GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
 CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
 CTCATAGACA AGGAGTTAGT GCCAATGGAA GCGGACGAGG AGCTGAAAT GCTCGCCTTC 420
 GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGCCCAAT CCTTATGATA 480
 AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACCTTGA AGAACGTGA TCTCCCTAC 540
 GTTGACGTCG`TCTCGACCGA GAGGAGATG ATAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
 AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGGACAAC TCGACTTCGC CTATCTGAAA 660
 AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
 ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAG GACGGATACA CTTGATCTC 780
 TATCCTGTGA TAAGACGAGC GATAAACCTG CCCACATACA CGCTGAGGC CGTTTATGAA 840
 GCCGTCCTCG GTCAGCCGAA GGAGAAGTT TACGCTGAGG AAATAACCAAC AGCCTGGGAA 900
 ACCGCGGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCCAA GGTACATAC 960
 GAGCTTGGGA AGGAGTTCTT TCCGATGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
 CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGTTCTT CCTCAGGAAG 1080
 GCCTATGAGA GGAATGAGCT GGGCCCGAAC AAGCCGATG AAAAGGAGCT GGCCAGAAGA 1140
 CGGCAGAGCT ATGAAGGAGG CTAATGTAATA GAGCCCGAGA GAGGTTGTG GGAGAACATA 1200
 GTGTACCTAG ATTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
 GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGAGT CGGCCACCGC 1320
 TTCTGCAAGG ACTTCCGAGG ATTTATCCCG AGCCTGCTTG GAGACCTCTT AGAGGAGAGG 1380
 CAGAAGATTA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
 TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
 AGGCGCGCT GGTACTGCAA GGAGTGTGA GAGAGCGTAA CGGCTGGGG AAGGAGTAC 1560
 ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGTAAAT CTACAGCGAC 1620
 ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
 ATGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGCGG CGCTTGAGCT CGAGTACGAG 1740
 GGCCTTCTACA AACCGGCTT CTTCGTCACG AAGAAGAAAT ATCGGTGAT AGACGAGGAA 1800
 GGCAAGATTA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
 GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTGA GAAGCCGCTG 1920
 AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
 GTGATCCACG AGCAGATAAC GAGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040

GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGAGGATA GGCACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGGCTTA CCAGAAGACG 2280
AGACAGGTTG GTTGAAGTGC TTGGCTGAAG CCGAAGGGA CT //TAG 2325

(HME-like)-Vent DNA POLYMERASE FUSION PROTEIN (Fig. 17-N)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

ATGATACTGG ACACTGATTA CATACAAAA GATGGCAAGC CTATAATCCG AATTTTAA 60
AAAGAGAACG GGGAGTTTAA AATAGAATT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAG ATGACTCCGC TATTGAGGAG ATAAGGCAA TAAAGGCGA GAGACATGA 180
AAAACGTGA GAGTGCTGA TGCAGTGAA GTCAGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGA AGCTCATTTT CGAGCATCCC CAAGACXXC CAGCTATGCG GGGCAATA 300
AGGGAACATC CAGCTGTGCT TGACATTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGCGTTGAT TCCCATGGAG GGAGACGAGG AGCTTAACT CTTGCCCTTT 420
GATATTGAAA CGTTTATCA TGAGGAGAT GAATTTGAA AGGCGAGAT AATATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAATG ATAAAGCCTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAATT TTGATTGGC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTCC CAGTTGTCCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAATT 840
TATGAAGCAG TTTTAGGAAA AACCAGAACG AAATTAGGAG CAGAGGAAT TGCCGCTATA 900
TGGAAGACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGAGTG GTATCTTTTA 1080
AGGTTGGCAT ACGCGAGGAA TGAAC TTGCA CCGAACAAAC CTGATGAGGA AGAGTATATA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAG AGCCAGAAAA AGTTTGTGG 1200

GAAAAATATCA TTTATTGGA TTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
 GTATCCCCAG ATACCCTTGA AAAAGAGGC TGTAGAATT AGCATGTTGC TCCGATAGTA 1320
 GGATATAGGT TCTGCAAGA CTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
 GCAATGAGGC AAGATATATA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
 ATGCTCGATT ATAGGCAAG GGTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
 GGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
 AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAA AGTTCGGCTT TAAGTTCTT 1620
 TATCGGACA CTGACGGCTT TTATGCCACA ATACCCGGG AAAAGCCTGA ACTCATTAAA 1680
 AAGAAAGCCA AGGAATCCT AACTTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
 GAGTATGAG GCTTTTACTT GAGAGGATTG TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
 GATGAAGAG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGAGAGA TTGAGTGAG 1860
 ATAGCTAAG AGACTCAGGC AAAGGTTTGA GAGGCTATAC TTAAGAGAGG AAGTGTGAA 1920
 AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAATAG CAAATACAG GTTCCACTT 1980
 GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTAA AGGACTACAA AGCCATTGGC 2040
 CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGA TAAAGTGAA ACCGGCACA 2100
 ATAATAAGCT ATATCGTCT CAAAGGAGC GGAAGATAA GCGATAGGT AATTTTACTT 2160
 ACAGAATACG ATCTTAGAAA ACACAAGTAC GATCCGACT ACTACATAGA AAACCAAGTT 2220
 TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGATACA GAAAGAGGA TTAAAGTAT 2280
 CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Vent DNA POLYMERASE - (HMF-like) FUSION PROTEIN (Fig. 17-0)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG AACTGATTA CATAACAATA GATGCAAGC CTATAATCCG AATTTTAAAG 60
 AAAGAGAACG GGGAGTTAA AATAGAATT GACCCTCATT TTCAGCCCTA TATATATGCT 120
 CTCTCAAAG ATGACTCCGC TATGAGGAG ATAAAGGCAA TAAAGGCCA GAGACATGGA 180
 AAAACTGTGA GAGTGTGGA TGCAGTGAAT GTCAGGAAA AATTTTGGG AAGGGAAGTT 240
 GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCC GGGCAAAATA 300
 AGGGAACATC CAGCTGTGTT TGACATTTAC GAATATGACA TACCCTTGC CAAGCGTTAT 360
 CTCATAGACA AGGCGTTGAT TCCCATGGAG GGAGACGAG AGCTTAAGCT CCTTGCCCTT 420
 GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTTGGA AGGCGAGAT AATAATGATT 480
 AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACAATGA AAAATATCGA TTTGCCGTAT 540
 GTGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
 AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660

AACGGGCAG AAAAGCTGGG AGTTGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
 CCCAAGATTG AGAGGATGGG TGATAGTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
 GATCTTTCC CAGTTGTGG AAGACGATA AACCTCCCA CGTATACGCT TGAGGCAGTT 840
 TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
 TGGAAACAG AAGAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGCA 960
 ACGTATGAGC TCGGAAGA ATTCTTCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
 CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGAGTG GTATCTTTTA 1080
 AGGTGGCAT ACCGAGGAA TGAAGTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAA 1140
 CGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAGA AGCCAGAAA AGTTTGTGG 1200
 GAAAAATATCA TTTATTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
 GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAGAATT ACGATGTTGC TCCGATAGTA 1320
 GGATATAGGT TCTGAAGGA CTTCCGGGC TTTATTCCCT CCATCTCGG GGACTTAATT 1380
 GCAATGAGGC AAGATATAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
 ATGCTCGATT ATAGGCAAG GGTATTAAA TTGCTTGCA ACAGCTATTA CGGTATATG 1500
 GGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
 AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCCGCTT TAAGTTCTT 1620
 TATCGGACA CTGACGGCTT TTATGCCACA ATACCAGGGG AAAAGCCTGA ACTCATTAAA 1680
 AAGAAGCCA AGGAATCCT AAACCTACATA AACTCCAAC TTCCAGGCTT GCTGAGCTT 1740
 GAGTATGAGG GCTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
 GATGAAGAGG GCAGGATAAC AACAGGGGC TTGGAAGTAG TAAGGAGAGA TTGAGTGAG 1860
 ATAGCTAAGG AGACTCAGGC AAAGTTTGA GAGCTATAC TTAAGAGAGG AAGTGTGAA 1920
 AAAGCTGTAG AAGTTGTAG AGATGTTGTA GAGAAATAG CAAATACAG GGTCCACTT 1980
 GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTAA AGGACTACAA AGCCATTGGC 2040
 CCTCATGTCG CGATAGCAAA AAGACTTCCC GCAAGAGGGA TAAAGTGAA ACCGGGCACA 2100
 ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATTA GCGATAGGGT AATTTACTT 2160
 ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
 TTGCCGGCAG TACTTAGAT ACTCGAAGCG TTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
 CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
 AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
 AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Deep Vent- (Hmf-1like) DNA polymerase fusion protein (Fig. 17-P)

Fig 17P (Cont)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG	ACGCTGACTA	CATCACCGAG	GATGGAAAG	CGATTATAAG	GATTTCAAG	60
AAAGAAAACG	GCGAGTTTAA	GGTTGACTAC	GACAGAAACT	TTAGACCTTA	CATTACGCT	120
CTCCTCAAG	ATGACTCGCA	GATTGATGAG	GTTAGGAAGA	TAACCGCCGA	GAGGCATGG	180
AAGATAGTGA	GAATTATAGA	TGCCGAAAAG	GTAAGGAAGA	AGTTCCTGGG	GAGCGGATT	240
GAGGTATGGA	GGCTGTACTT	TGAACACCCCT	CAGGACXXXC	CCGCAATAAG	GGATAAGATA	300
AGAGAGCATT	CCGCAGTTAT	TGACATCTTT	GAGTACGACA	TTCCGTTCCG	GAAGAGGTAC	360
CTAATAGACA	AAGGCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGGCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCCAAAGTC	ATAACGTGA	AAAAGATCGA	TCTCCCGTAC	540
GTCGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCCGT	TCCTCAAGGT	GATAAGGGAG	600
AAAAGATCCC	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGCTCGG	GATPAAAGCTA	CCCCCTGGGA	GGGACGGTAG	TGAGCCAAAG	720
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAGAAAGTT	TACGCTCACC	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAGG	GACTGGAGAG	AGTTGCAAG	TATTCATGG	AGGATGCAAA	GTTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGTACTCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAAATGAAT	GGCTCCAAAC	AAGCCGGATG	AGAAGGAGTA	CGAGAGAAAG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCA	GAGCCTGTAC	CCCTCGATTA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCCGCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAATAAGGAA	GATGAAGCT	TCTAAGAGCC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAAACAGCT	ATTATGGTA	TTATGGGTAC	1500
GCAAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAACGTGAG	GAAAAGTTCC	GGTTCAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAAGAAA	1680
GCCCTAGAGT	TCGTAAGATTA	TATAAACGCC	AAGCTCCAG	GGCTGTTGA	GCTTGAGTAC	1740
GAGGCTTCT	ACGTGAGAGG	GTTCTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAAGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAAGAAACC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAGAGATAG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCTT	TGCAGAGGAG	2160

TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220
 GCCGTTCTTA GAATATTAGA GGCCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
 ACTAACAAGA CAGGCTTAC GGCATGCTT AACATCAAGA AGAAG // 2328

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
 AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
 AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

(Hmflike) - Deep Vent DNA polymerase fusion protein (Fig. 17-Q)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
 AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
 AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

//ATGATCTTG ACGCTGACTA CATCACCAG GATGGGAAGC CGATTATAAG GATTTCAG 60
 AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTACGCT 120
 CTCCTCAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCGA GAGCATGGG 180
 AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGCCGATT 240
 GAGGTATGGA GGCTGTACTT TGAACACCCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
 AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCCG GAAAGAGTAC 360
 CTAATAGACA AAGGCCCTAAT TCCAATGGAA GCGCATGAAG AGCTCAAGTT GCTCGCATTT 420
 GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGCCCAT TATAATGATA 480
 AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGA AAAAGATCGA TCTCCCGTAC 540
 GTCGAGTAG TTTCACGCGA GAGGAGATG ATAAAGCGGT TCCTCAAGGT GATTAAGGAG 600
 AAAGATCCCG ATGTTATTAAT TACCTACAAC GGCAGTTCTT TCGACCTTCC CTATCTAGTT 660
 AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGCTAG TGAAGCAAAG 720
 ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATTAAGG GAAGGATPACA CTTTGACCTC 780
 TACCACGTGA TTAGGAGAAG GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG 840
 GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCAG AGATAGCTGA GGCTGGGAG 900
 ACTGGAAGG GACTGAGAG AGTTGCAAG TATTCAATGG AGGATGCAAA GGTAACTGAC 960

GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGTTAGT CGGCCAGCCC 1020
 CTGTGGGATG TTTCTAGGTC TTCACTGGC AACTTGGTGG AGTGTACTT CCTCAGGAAG 1080
 GCCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGAGTA CGAGAGAAGG 1140
 CTAAGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAGGGCT CTGGAGGGG 1200
 TTAGTTCCC TAGATTTCAG GAGCCTGTAC CCTCGATTA TAATCACCCTA TAACGTCTCA 1260
 CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTGGGCAC 1320
 AAGTTCTGCA AGGACTTCCC GGGGTTATC CCCAGCCTGC TCAAGAGGTT ATTGATGAA 1380
 AGGCAAGAAA TAAAAAGGAA GATGAAGCT TCTAAGACC CAATCGAGAA GAAGATGCTT 1440
 GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAAACAGCT ATTATGGTA TTATGGTAC 1500
 GCAAAAAGCCC GTTGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGAA 1560
 TATATAGAGT TCGTAAGGAA GGAAGTGGAG GAAAGTTCCG GGTTCAAAGT CTTATACATA 1620
 GACACAGATG GACTCTACGC CACAATTCTT GGGGCAAAAC CCGAGAGAT AAAGAAGAAA 1680
 GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCAG GGTGTTGA GCTTGAGTAC 1740
 GAGGCTTCT ACGTGAGAGG GTTCTCGTG ACGAAGAGA AGTATGCGTT GATAGATGAG 1800
 GAAGGGAAGA TAATCACTAG GGGGCTTGA ATAGTCAGA GGGACTGGAG CGAATAGCC 1860
 AAAGAAAACC AAGCAAAAGT CCTAGAGGCT ATCCTAAGC ATGCCAACGT TGAAGAGGCA 1920
 GTAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAAG 1980
 CTAGTTATTT ACGAGCAGAT CACGAGGCC CTTACGAGT ACAAGGCTAT AGTCCGCAC 2040
 GTTGCCGTGG CAAAAAGGTT AGCCGCTAGA GGAGTAAAG TGAAGCCTGG CATGGTATA 2100
 GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
 TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAAATCA GGTTTTACCT 2220
 GCCGTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
 ACTAACAGA CAGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA 2328

JDE-3 - (Hmf-like) fusion protein (Fig. 17-R)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACGAGAAATGAAAGCCCGTCATCAGGTTCTTCAAGAAGAGAACGGCGAGTTCAAGATTGAATACGACCGCGAGTTGAGCCCTACTTCT
 ACGCGCTCTCAGGAGCACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGAGAGGCAAGGAGGTTAAGGTTAAGCGCGGAGAGAGGTGAAGAAAAGTTCCCTCGG
 CAGGCTGTGAGGTTCTGGTCTCTACTTCAAGCAACCGCAGGACX~~XXXX~~CCGCAATCCGACAAATAAGGAAGCAACCGCGGTCAATGACATCTACGAGTACGACATACCC
 TTGCGCAAGCGCTACCTCATAGACAAGGCGCTAATCCGATGGAAGGTGAAGAGCTTAACTCATGTCTT~~GAC~~AT~~GAG~~ACGCTCTAACCAAGGAGGAAGAGTTTGAA
 CCGGCGCGATTCTGATGATAAGCTACGCGGATGAAGCGAGGCGCGGTGATAACCTGGAAGAAGATCGACCTTCTTACGTTGAGGTTGTCTCCACCGAGAAGAGATGATTAA
 GCGCTTCTTGAGGTCGTTAAGGAAGAACCCGACGTGCTGATAACATACAACGCGCAACTTCGACTTCGCTACCTGA~~AAAA~~AGCGCTGTGAGAAGCTTGCGGTGAGCTTT
 ACCCTCGGAGGAGCGGAGCGGAGCGGAAGATACGCGCATGGGGACAGGTTTGGGTCGAGGTGAAGGCGAGGTTACACTTTCGACCTTTATCCAGTCA~~TAAG~~CGCACCATAA

ACCTCCCGACCTACACCCCTTGAGGCTGTATACGAGCGGCTTTTCGCAAGCCCAAGGAGAAGTCTACGCCGAGAGATAGCCACCGCCTGGAGACCGGAGGGCTTGAGAG
GGTGGCGGCTACTCGATGAGGAGCGGAGGGTTACCTACGAGCTTGGCAGGAGTTCTCCGATGAGGCCAGCTTTCAGGCTCATGGCCAAGGCTCTGGGACGTTTCC
CGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCCTCTAAGGAAGCCCTACGAGAGAACGAACTCGCTCCCAACAAGCCCGACGAGAGGAGCTGGCGAGGAGAAGGGGGCT
ACGCCGGTGGCTACGTCAAGGAGCGCGGAGCTGTGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTACCCCTTCAATCAATAATCACCCACAACGCTCTCGCCAGATAC
GCTCAACCGCGAGGGGTGTAGAGCTACGACGTTGCCCGGAGGTGCTCACAAGTTCTGCAAGGACTTCCCGGCTTCATTCGAGCCTGCTCGAAACCTGCTGAGGAAAGG
CAGAAGATAAAGAGAGATGAAGCAACTCTCGACCCGCTGAGAGAATCTCTCGATTACAGGCAACGCGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT
ATGCCAGGGCAAGATGGTACTGCAGGAGTGGCCCGAGAGCGTTACGGCATGGGGAAGGAGTCAATCGAAATGGTCAATCAGAGAGCTTGAGGAAAAGTTCGGTTTAAAGTCC
CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGACGCTGAACAGTCAAGAAAAGCAATGAGTTCTTAACTATATCAATCCCAACTGCCCGCCTTCTC
GAACTCGAATACGAGGGCTTCTACGTCAAGGGCTTCTTCGTACGAAAGAAAAGTACCGCGGTCAATCGAGAGAGGCGCAAGATAACACCGCGGGCTTGAGATAGTCAAGCGCG
ACTGAGCGAGATAGCGAAGGAGACGCGAGGGTTTGGAGCGGATCTCAGGCCACGGTGAAGAGCGCTCAGAAATGTGAGAGCGCTCAGAAATGTGAGAGAGTCAACGAAAGCTGAGCAA
GTACGAGGTTCCCGCGAGAGCTGTTATCCACGAGCAGATAACGCGAGCTCAAGGACTACAGGCCACCGCGCCGACGTAGCCATAGCCGAAAGCTTTGGCCGCAAGAGT
GTTAAATCCGGCCGGAACGTGTATAGCTACATCGTTCTTGAAGGCTCCGGAAGGATAGGCGACAGGGCGAATTCCTTCGACGAGTTGACCCGACGAAAGCAAGTACGATG
CGACTACTACATCGAGAACCAAGGTTCTGCCGCGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGAGACCTGCGCTACCAAGAGACGAGGACAGGTCGGCTTGGCGC
GTGGCTGAAGCCGAAGGGGAAGAAGAAG//

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

(Hmf-like) - JDF-3 fusion protein (Fig. 17-S)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACCGGAGTTCAAGATTGAATACGACCGGAGTTGAG
CCCTACTTCTACGCGCTCTCAGGAGCACTCTGCCATCGAAGAAATCAAAAAGATAACCGGAGAGCAAGGAGGTCCTTAAGTTAAGCGCGGAGAGAGT
GAAGAAAAAGTTCCTCGGAGGTTCTGTGAGGTTGGGTCCTTACTTACGCAACCGCAGGACXXXCCGCAATCCGGAACAATAAGGAAGCAACCGCGGTCA
TCGACATCTACGAGTACGACATACCCCTTCGCCAAGCGCTACCTCATAGACAAGGCCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTTCCGACATC
GAGACGCTCTACCAAGGAGAGAGATTGGAAACCGGCGGATTTCTGATGATAAGCTACCGCGATGAAGCGAGGCGCGGTGATTAACCTGGAAGAGATCGACCT
TCCTTACGTTGAGGTTGTCTCCACCAGAGAGAGATGATTAAAGCGCTTCTGAGGGTCTTAAGGAGAAAGACCGGACGTGCTGATTAACATACACGCGCAACT

Fig 17S (cont)

TCGACTTCGCCCTACCTGAAAAAGCGCTGTGAGAAGCTTGCCGTGAGCTTTACCCCTCGGAGGGACGGGAGCCGGAAGATACAGCGCATGGGGACAGGTTTGGC
GTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCATAAGCGGCACCATATAACCTCCGAGACTACACCCCTTGAGGCTGTATACGAGCGGTTTTCGGCAA
GCCAAGGAGAAGGTTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGGCTTGAGAGGGTCCGGCTACTCGATGGAGACCGGAGGGTTACCTACG
AGCTTGGCAGGGAGTTCTTCCGATGGAGGCCCAAGCTTTCAGGCTCATCGGCCAAGGCCCTTGGAAGCTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTC
CTCCTAAGGAAGGCTACGAGAGGAACGAACCTCGCTCCCAACAAGCCGACGAGAGGAGCTGGCGAGGAAGGGGGGCTACgCCGGTGCTACGTCAAGGAGCC
GGAGCGGGGACTGTGGACAATAATCGTGTATCTAGACTTTCGTAAGTCTTACCCCTTCAATCATATCACCCACAACGTTCTCGCCAGATAAGCTCAACCGGAGGGGT
GTAGAGCTACGACGTTGCCCCGAGGTCGGTCAACAAGTTCTGCAAGGACTTCCCCGGCTTCATTTCCGAGCCTGCTCGGAACCTGCTGGAGGAAGGCAGAAGATA
AAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGATTACAGGCAACGGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTA
TGCCAGGGCAAGATGGTACTGCAAGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGAGTACATCGAAATGGTCATCAGAGAGCTTGAGGAAGTTCGGTTTTA
AAGTCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAACAAGTCAAGAAAAAGGCAATGGAGTCTTAACTATATCAATCCCAA
CTGCCCGGCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAAGGGCTTCTTGTCACGAAGAAAAAGTACGCGGTTCATCGACGAGGAGGCAAGATAACCAAGCG
CGGCTTGAGATAGTCAAGGCGGACTGGAGCGAGATAGCGAAGGAGACCGAGCGGAGGTTTGGAGGCGATPACTCAGGCCACGGTGAAGAGGCGCTCAGAA
TTGTCAAGGAAGTCAACCGAAAAAGCTGAGCAAGTACGAGTTCGCCCGGAGAAGCTGTTATCCACGAGCAGATAACGCGGAGCTCAAGGACTACAAGGCCACCGGC
CCGCACGTAGCCATAGCGGAAGCGTTTGGCCGCCAGAGGTGTTAAATCCGGCCCGGAACGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGCGGACAG
GGGATTTCCCTTCGACGAGTTGACCCCGACGAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCG
GCTACCGCAAGGAAGACCTGCGCTACCAAGAAGACGAGCGAGTCCGGCTTGGCGCGTGCTGA

ACCESSION No: AE010210 REGION: complement (8333..9082) (Fig. 17-T)
/product="pcna sliding clamp (proliferating-cell nuclear antigen)"

M	P	F	E	I	V	F	E	G	A	K	E	F	A	Q	L	I	D	18
ATG	CCA	TTT	GAA	ATC	GTA	TTT	GAA	GGT	GCA	AAA	GAG	TTT	GCC	CAA	CTT	ATA	GAC	54
T	A	S	K	L	I	D	E	A	A	F	K	V	T	E	D	G	I	36
ACC	GCA	AGT	AAG	TTA	ATA	GAT	GAG	GCC	GCG	TTT	AAA	GTT	ACA	GAA	GAT	GGG	ATA	108
S	M	R	A	M	D	P	S	R	V	V	L	I	D	L	N	L	P	54
AGC	ATG	AGG	GCC	ATG	GAT	CCA	AGT	AGA	GTT	GTC	CTG	ATT	GAC	CTA	AAT	CTC	CCG	162
S	S	I	F	S	K	Y	E	V	V	E	P	E	T	I	G	V	N	72
TCA	AGC	ATA	TTT	AGC	AAA	TAT	GAA	GTT	GTT	GAA	CCA	GAA	ACA	ATT	GGA	GTT	AAC	216
M	D	H	L	K	K	I	L	K	R	G	K	A	K	D	T	L	I	90
ATG	GAC	CAC	CTA	AAG	AAG	ATC	CTA	AAG	AGA	GGT	AAA	GCA	AAG	GAC	ACC	TTA	ATA	270
L	K	K	G	E	E	N	F	L	E	I	T	I	Q	G	T	A	T	108
CTC	AAG	AAA	GGA	GAG	GAA	AAC	TTC	TTA	GAG	ATA	ACA	ATT	CAA	GGA	ACT	GCA	ACA	324
R	T	F	R	V	P	L	I	D	V	E	E	M	E	V	D	L	P	126
AGA	ACA	TTT	AGA	GTT	CCC	CTA	ATA	GAT	GTA	GAA	GAG	ATG	GAA	GTT	GAC	CTC	CCA	378
E	L	P	F	T	A	K	V	V	V	L	G	E	V	L	K	D	A	144
GAA	CTT	CCA	TTC	ACT	GCA	AAG	GTT	GTA	GTT	CTT	GGA	GAA	GTC	CTA	AAA	GAT	GCT	432
V	K	D	A	S	L	V	S	D	S	I	K	F	I	A	R	E	N	162
GTT	AAA	GAT	GCC	TCT	CTA	GTG	AGT	GAC	AGC	ATA	AAA	TTT	ATT	GCC	AGG	GAA	AAT	486
E	F	I	M	K	A	E	G	E	T	Q	E	V	E	I	K	L	T	180
GAA	TTT	ATA	ATG	AAG	GCA	GAG	GGA	GAA	ACC	CAG	GAA	GTT	GAG	ATA	AAG	CTA	ACT	540
L	E	D	E	G	L	L	D	I	E	V	Q	E	E	T	K	S	A	198
CTT	GAA	GAT	GAG	GGA	TTA	TTG	GAC	ATC	GAG	GTT	CAA	GAG	GAG	ACA	AAG	AGC	GCA	594
Y	G	V	S	Y	L	S	D	M	V	K	G	L	G	K	A	D	E	216

TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
V T I K F G N E M P M Q M E Y Y I R	234
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
D E G R L T F L L A P R V E E *	250
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA	750

(PCNA)-Taq DNA polymerase fusion protein (Fig. 17-U)

M P F E I V F E G A K E F A Q L I D	18
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
T A S K L I D E A A F K V T E D G I	36
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
S M R A M D P S R V V L I D L N L P	54
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
S S I F S K Y E V V E P E T I G V N	72
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
M D H L K K I L K R G K A K D T L I	90
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
L K K G G E E N F L E I T I Q G T A T	108
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
R T F R V P L I D V E E M E V D L P	126
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
E L P F T A K V V V L G E V L K D A	144
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
V K D A S L V S D S I K F I A R E N	162
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486

Fig 17U (cont)

E F I M K A E G E T Q E V E I K L T	180
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
L E D E G L L D I E V Q E E T K S A	198
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
Y G V S Y L S D M V K G L G K A D E	216
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
V T I K F G N E M P M Q M E Y Y I R	234
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
D E G R L T F L L A P R V E E	250
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG	
G G G	
// GGC GGC GGT	
V T S G M L P L F E P K G R V L L V	
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG	
D G H H L A Y R T F H A L K G L T T	
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC	
S R G E P V Q A X Y G F A K S L L K	
AGC CGG GGG GAG CCG GTG CAG GCG CTC TAC GGC TTC GCC AAG AGC CTC CTC AAG	
A L K E D G D A V I V V F D A K A P	
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC	
S F R H E A Y G G Y K A G R A P T P	
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC GCC CCC ACC CCA	
E D F P R Q L A L I K E L V D L L G	
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTC GGG	

Fig 17v (cont)

L A R L E V P G Y E A D D V L A S L
 CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG
 A K K A E K E G Y E V R I L T A D K
 GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA
 D L Y Q L L S D R I H V L H P E G Y
 GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC
 L I T P A W L W E K Y G L R P D Q W
 CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG
 A D Y R A L T G D E S D N L P G V K
 GCC GAC TAC CGG GCC CTC ACC GCG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG
 G I G E K T A R K L L E E W G S L E
 GGC ATC GGG GAG AAG ACG GCG AAG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA
 A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG
 A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
 L P L E V D F A K R R E P D R E R L
 CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
 L E S P K A L E E A P W P P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC
 F V G F V L S R K E E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
 L A A A R G G R V H R A P E P Y K A
 CTG GCC GCC GCC AGG GGG GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC

Fig 17v (cont)

L R D L K E A R G L L A K D L S V L
 CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
 A L R E G L G L P P G D D P M L L A
 GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
 Y L L D P S N T T P E G V A R R Y G
 TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
 G E W T E E A G E R A A L S E R L F
 GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC
 A N L W G R L E G E E R L L W L Y R
 GCC AAC CTG ATG GGG AGG CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG
 E V E R P L S A V L A H M E A T G V
 GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG
 R L D V A Y L R A L S L E V A E E I
 CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
 A R L E A E V F R L A G G H P F N L N
 GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC
 S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC
 G K T E K T G K R S T S A A V L E A
 GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTG GAG GCC
 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC
 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG
 G R L H T R F N Q T A T A T G R L S

Fig 17 U (Cont)

GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC ACG GGC AGG CTA AGT
 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG
 I R R A F I A E E G W L L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT
 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC
 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC
 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC GGC AAG ACC ATC
 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC
 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC
 K V R A W I E K T L E E G R R G Y
 AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AAG AGG CGG GGG TAC
 V E T L F G R R R Y V P D L E A R V
 GTG GAG ACC CTC TTC GGC CGC CGC CTG TAC GTG CCA GAC CTA GAG GCC CGG GTG
 K S V R E A A E R M A F N M P V Q G
 AAG AGC GTG CGG GAG GCC GCG GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
 T A A D L M K L A M V K L F P R L E
 ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
 E M G A R M L L Q V H D E L V L E A
 GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC

P K E R A E A V A R L A K E V M E G
 CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

 V Y P L A V P L E V E V G I G E D W
 GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG
 L S A K E G I D G R G G G G H H H H
 CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGC CAT CAT CAT CAT

 H H *
 CAT CAT TAA

Taq DNA polymerase-(PCNA) fusion protein (Fig. 17-V)

G G G
 // GGC GGC GGT

V T S G M L P L F E P K G R V L L V
 GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

 D G H H L A Y R T F H A L K G L T T
 GAG GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

 S R G E P V Q A X Y G F A K S L L K
 AGC CGG GGG GAG CCG GTG CAG GCG OTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

 A L K E D G D A V I V V F D A K A P
 GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

 S F R H E A Y G G Y K A G R A P T P
 TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACC CCA

 E D F P R Q L A L I K E L V D L L G
 GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

Fig 17v (cont)

L A R L E V P G Y E A D D V L A S L
 CTG GCG CGC CTC GAG GTC CCG GCG TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG
 A K K A E K E G Y E V R I L T A D K
 GCC AAG AAG GCG GAA AAG GAG GCG TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA
 D L Y Q L L S D R I H V L H P E G Y
 GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC
 L I T P A W L W E K Y G L R P D Q W
 CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG
 A D Y R A L T G D E S D N L P G V K
 GCC GAC TAC GGG GCC CTC GAC ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG
 G I G E K T A R K L L E E W G S L E
 GGC ATC GGG GAG AAG ACC GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA
 A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG
 A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
 L P L E V D F A K R R E P D R E R L
 CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
 L E S P K A L E E A P W P P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC
 F V G F V L S R K E E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
 L A A A R G G R V H R A P E P Y K A

Fig 17 v (cont)

CTG GCC GCC GCC AGG GGG GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
Y L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC GCC CTT TCC GAG AGG CTC TTC
A N L W G R L E G E E R L L W L Y R
GCC AAC CTG TGG GGG AGG AGG CTT GAG GGG GAG GAG AGG CTC CTT TGG CTT TAC CGG
E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG
R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
A R L E A E V F R L A A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC
S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC
G K T E K T G K R S T S A A V L E A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC GTC CTG GAG GCC
L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC
K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

9811/LL

Fig. 17v (cont)

G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC ACG GGC AGG CTA AGT
S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG
I R R A F I A E E G W L L V A L D Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT
S Q I E L R V L A H L S G D E N L I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC
R V F Q E G R D I H T E T A S W M F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC
G V P R E A V D P L M R R A A K T I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC
N F G V L Y G M S A H R L S Q E L A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC
I P Y E E A Q A F I E R Y F Q S F P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC
K V R A W I E K T L E E G R R G Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC
V E T L F G R R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
K S V R E A A E R M A F N M P V Q G
AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
T A A D L M K L A M V K L F P R L E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAG GAG CTG GTC CTC GAG GCC

981/86

V	K	D	A	S	L	V	S	D	S	I	K	F	I	A	R	E	N	162
GTT	AAA	GAT	GCC	TCT	CTA	GTG	AGT	GAC	AGC	ATA	AAA	TTT	ATT	GCC	AGG	GAA	AAT	486
E	F	I	M	K	A	E	G	E	T	Q	E	V	E	I	K	L	T	180
GAA	TTT	ATA	ATG	AAG	GCA	GAG	GGA	GAA	ACC	CAG	GAA	GTT	GAG	ATA	AAG	CTA	ACT	540
L	E	D	E	G	L	L	D	I	E	V	Q	E	E	T	K	S	A	198
CTT	GAA	GAT	GAG	GGA	TTA	TTG	GAC	ATC	GAG	GTT	CAA	GAG	GAG	ACA	AAG	AGC	GCA	594
Y	G	V	S	Y	L	S	D	M	V	K	G	L	G	K	A	D	E	216
TAT	GGA	GTC	AGC	TAT	CTC	TCC	GAC	ATG	GTT	AAA	GGA	CTT	GGA	AAG	GCC	GAT	GAA	648
V	T	I	K	F	G	N	E	M	P	M	Q	M	E	Y	Y	I	R	234
GTT	ACA	ATA	AAG	TTT	GGA	AAT	GAA	ATG	CCC	ATG	CAA	ATG	GAG	TAT	TAC	ATT	AGA	702
D	E	G	R	L	T	F	L	L	A	P	R	V	E	E	*			250
GAT	GAA	GGA	AGA	CTT	ACA	TTC	CTA	CTG	GCT	CCA	AGA	GTT	GAA	GAG	TGA			

Pfu DNA Polymerase (WT) -(PCNA) fusion protein (Fig. 17-W)

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ccctggtcct gggccacat atatgttctt actgcctt atgaagaatc ccccaagtcgc
tctaaccctgg gttatagtga caaatcttcc tccaccaccgg cccaagaag tlatltctat
caactctaca cctcccttat ttctctctt atgagattt taagtatagt tatagagaag
gttttact ccaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggtattc aaaaaagaga acggaattt
taagatagag catgatagaa cttttaagcc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaagggcat ggaagattg tgagaattgt
tgatgtagag aaggttgaga aaagtcttct cggaagcct attaccgtgt ggaacttta

Fig 17W (cont)

tttggaacat ccccaagatg ttcccatat tagagaaaa gttagagaac atccaagcagt
tgtggacatc ttcgaatcag atatccatt tgcгаааgаgа таасааgссс
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcacgaaagg аааgаgttg gaaaaggccc aattataatg atagttatg cagatgaaaa
tgaaagcaag gtgattact ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaaact
tgggatttaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaaagaa acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggcgttatat gaagcaattt ttggaaggcc
aaaaggagag gtatacgccg acgagatagc aaaaagcctgg gaaagtggag agaaccctga
gagagttgcc aaatactcga tggaaagatgc aaaggcaact tatgaaactcg ggaagaaat
cctccaatg gaaattcagc ttccaagatt agttggacaa ccttatggg atgtttcaag
gtcaagcaca gggaaacctg tagagtgtt ctacttagg aaagcctacg aaagaaaacga
agtagctcca aacaagccaa gtgaaagagg gtatcaaaga aggcctcagg agagctacac
aggtggttc gttaaaggag cagaaaaggg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaattct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctgtttt атасааgтс тсttggaca ttgttagag gaaagacaaa agatlaagac

86/18

Fig 17w (cont)

aaaaatgaag gaaactcaag atcctataga aaaaatactc ctgactata gacaaaagc
gataaaactc ttagcaaat cttctacgg atattatgc tatgcaaaag caagatgta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttaagtatg
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atgtctcta
tgcaactatc ccaggagagag aaagtgaaga aataaagaaa aaggctctag aattgtaaa
atacataaat tcaaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag
gggatcttc gttacgaaga agaggtatgc agtaatagat gaagaaagaa aagtcattac
tcgtggttta gagatagtta ggagagatlg gagtgaaat gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaaaga gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaaaga
actagctgct aaaggagtta aaataaagcc aggaatgta attgataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctaagttag gaatcacgac ccaaaaagca
caaagtatgac gcagaatat accattgagaa ccaggttctt ccagcggtac ttagatat
ggaggatctt ggatcacgaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatla aaaaatccta gaaaagcgat agatalcacac tttattctt
tctaaccctt ttctatgaa gaagaaactga gcaggaattla ccagttcttc cgttatttta
tgggtaatta aaaaaccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaatggt

Fig. 17W (cont)

ctatctgcac gcttctcttg ctcggaanng gaggtatcat aacaacagta tcaacattct
cagaagattg agaaacatca gaaacttga cttctacaac atttctaact ttgcaactct
tcaagattt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt
tttgctccaa gcagagccgc tccaatgat aacacccctg ttcccgacc caagtccgct
acaattttt ccttgatct cctaattat aagcaagcca aaggagagta gatgctacct
ttccggagat ttgtatctgc tctagccaag gtttggatt ttgaatcct ttaactctg
aaagtataat ttcaagctcc ttcttctca tgacagatga aaaattgtt tgtctcttt
taacttttac agaataact gtctcaaat atgacaactc ttgacatttt tacttcat
ccagggtaat gtttttaagt atgaatttt tcttcatag aggaggnnn ngtcctctc
ctcgatttcc ttggtgtgc tccatatgat aagcttccaa agtgggtgt cagactttta
gacactcaaa taccagacga caatggtgtg ctcaactcaag ccccatatg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgtgtagc tcntccnga
aagattgaga tgttcttg //

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594

TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
 GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
 GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

(PCNA) - Pfu DNA Polymerase (WT) fusion protein (Fig. 17-X)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
 ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
 AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
 TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
 ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
 CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
 AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
 GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
 GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
 GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
 CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
 TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
 GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
 GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG

//

ccctggtcct gggccacacat atatgttctt actgccttt atgaagaatc ccccaagtcgc
 tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
 caactctaca cctcccttat tttctctctt atgagatttt taagtatagt tatagagaag
 gtttttact ccaaaactgag ttagtagata tgtggggagc ataatgatlt tagatgtgga
 ttacataact gaagaaggaa aacctgttat taggtatctc aaaaaagaga acggaaaatt
 taagatagag catgatagaa ctlttagacc atacatttac gctcttctca gggatgatc
 aaagattgaa gaagttaaga aaataacggg ggaagggcat ggaagatttg tgagaattgt

Fig 17.X (cont)

tgatgtagag aaggttgaga aaaagttct cggcaagcct attacggtgt ggaacttta
tttggaaacat ccccaagatg ttcccatat tagagaaaaa gtagagAAC atccagcagt
tgtgacatc ttcgaatacg atatccatt tgcAaagaga taccatcgc acaaaagcct
aataccaatg gagggggaag aagagctaaa gattcttgc ttcgatatag aaaccctcta
tcaacgaagga gaagagtttg gaaaaagccc aattataatg atagtatg cagatgaaaa
tgaaagcaaa gtgattactt ggaaaaaaat agatcttcca tacgttgag ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcag gagaaagatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaatagcgga
tatgacggct gtagaagtca agggaaagaat acatttcgac ttgtatcatg taataacaag
gaacaataat ctccaacat acacactaga ggtgtatat gaagcaattt ttggaagccc
aaagugagag gtatacgccg acgagatagc aaagccctgg gaagtggag agaaccctga
gagagttgcc aaatactcga tggaaagatgc aaagccaact tatgaactcg gaaagaat
cctccaatg gaaattcagc ttccaagatt agttgacaa ccttatggg atgttcaag
gtcaagcaca gggaaccttg tagagtgtt ctacttagg aaagcctacg aaagaaacga
agt agctcca aacaagccaa gtgaagagga gtatcaaga aggtctcagg agagctacac
aggtggttc gttaagagc cagaaaaagg gtgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccaaatgtt tctccgata ctctaattct
tgagggatgc aagaactatg atatcgctcc tcaagtagc cacaagttct gcaaggacat

Fig 17X (cont)

ccctggttt ataccgaagtc tcttgggaca ttgttagag gaaagacaaa agatlaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttagctata gacaaaaagc
gataaaactc ttagcaaat cttctacgg atatgatgc tatgcaaaag caagatggtta
ctgtaaaggag tgtgctgaga gcgtactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaagt ttggttta agtcctctac attgacactg atgtctcta
tgcaactatc ccaggaggag aaagtgaaga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag
gggattcttc gttaa^ggaaga agaggtatgc agtaatagat gaagaaagaa aagtcattac
tcgtgttta gagatagtta ggaagatg gagtgaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaaaga gctgtgaga tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gatagtcct cacgtagctg ttgcaaaaga
actagctgct aaaggagtta aaataaagcc aggaatggtta attgataca tagtacttag
aggcgtggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatat acattgaga ccaggttctt ccagcggtac ttaggatatt
ggagggattt ggatcacgaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatla aaaaatccta gaaaagcgat agtatcaac ttatttctt
tctaaccctt ttctatgaa gaagaactga gcaggaatla ccagttcttc cgtatttta
tggttaatla aaaaccatg ctcttggag aatcttcgaa taaatccct aacttcaggc

ttgtctaagt gaatagaata aacaacatca ctcaactcaa acgccttcgt tagaatggt
 ctatctgcac gcttctctgg ctcggaanng gaggttcat aacaacagta tcaacattct
 cagaagaattg agaaacatca gaaactttga ctctacaac attctaact ttgcaactct
 tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa ttgcacgac gtagatcttt
 ttgtctccaa gcagagccgc tccaatgcat aacacccctg ttcccgacc caagtccgct
 acaattttt ccttgtatct cctaattgtat aagcaagcca aaggagagta gatgctacct
 ttccgggagc ttgtattgc tctagccaag gtttgggatt ttgtaacct ttaactctgg
 aaagtataat ttcaagctcc ttcttctca tgacagatga aaaattgttt tgtctcttt
 taactttac agaataact gtctcaatt atgacaactc ttgacatttt tacttcat
 ccagggtaat gtttttaagt atgaatttt tcttcatag aggaggnnn ngtcctctc
 ctgatttcc ttggtgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta
 gacctcaaa taccagacga caatggtgtg ctcaactcaag ccccatatg gttgagaaaa
 gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgtgtagc tcntccnnga
 aagattgaga tgttcttg // TGA

(PCNA) - PFU DNA POLYMERASE (V93 R OR E) fusion protein (Fig. 17-Y)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
 ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108

Fig 17Y (cont)

AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //

//ATGATTTT³AG ATGTGATTA CATACTGAA GAAGGAAAC CTGTTATTAG GCTATTCAA 60 AAAGAGACG GAAATTAA GATAGGCAT
GATAGACTT TTAGACCATA CATTACGCT 120 CTCTCAGGG ATGATTCAA GATTGAGAA GTTAAGAAA TAACGGGGG AAGCATGGA 180
AAGATTGTGA GAATTGTGA TGTAGAGAA GTTGAGAAA AGTTTCTCG CAAGCCTATT 240 ACCGTGTGA AACTTTATT GGAACATCCC
CAAGATXXXC CCACTATTAG AGA³AAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
CTCATCGACA AAGCCTAAT ACCAATGAG GGGAGAGAA AGCTAAAGAT TCTTGCCCTC 420 GATATAGAAA CCTCTATCA CGAAGAGAA
GAGTTTGAA AAGGCCCAAT TATAATGATT 480 AGTTATGAG ATGAAATGA AGCAAAGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTG TATCAAGCGA GAGAGAGATG ATAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTCCT ATATTAGCG 660 AAAAGGCGAG AAAA³ACTTG GATTAAATTA ACCATTGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGCGATAT GACGCTGTA GAAGTCAAG GAAGAATACA TTTGACTTG 780 TATCATGTAA TAACAAGGAC AATAATCTC
CCAACATACA CACTAGAGC TGTATATGAA 840 GCAATTTTG GAAAGCCAA GGAGAAAGTA TACGCCGACG AGATAGCAA AGCCTGGAA 900
AGTGAGAGA ACCTTGAGAG AGTTGCCAA TACTCGATGG AAGATGCAA GGCACTTAT 960 GAACTCGGA AAGAATTCT TCCAATGAA
ATTGAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGATG TTTCAAGTC AAGCACAGGG AACCTTGTAG AGTGGTCTT ACTTAGGAAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAC AAGCCAAGTG AAGAGAGTA TCAAGAAGG 1140 CTCAGGAGA GCTACACAGG
TGGATTGCTT AAAGAGCCAG AAAAGGGGT GTGGAAAAC 1200 ATAGTATACC TAGATTTAG AGCCCTATAT CCCTGATTA TAATTACCA
CAATGTTCT 1260 CCCGATATC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCTCA AGTAGCCAC 1320 AAGTTCTGA
AGGACATCCC TGGTTTATA CCAAGTCTCT TGGACATTT GTTAGAGAA 1380 AGACAAAGA TTAAGACAAA AATGAAGGA ACTCAAGATC
CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAATTCTT TCTACGATA TTATGCTAT 1500
GCAAAAGCAA GATGTA³CTG TAAGAGTGT GCTGAGAGCG TTA³CTGCTG GGAAGAAG 1560 TACATCGAGT TAGTATGAA GAGCTCGAA
GAAAAGTTG GATTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCA GAGGAGAAA GTGAGGAAT AAAGAAAAAG
1680 GCTCTAGAT TTGTAAATA CATTAATTCA AAGCTCCCTG GACTCTAGA GCTGAATAT 1740 GAAGGTTT ATAAGAGGG
ATTCTTCGTT ACGAAGAAGA GGTATGAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGA GAGATTGGAG
TGAATTGCA 1860 AAAGAAATC AAGCTAGAGT TTTGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920 GTGAGAATAG
TAAAGAAGT AATACAAAAG CTGCCAATT ATGAATTC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAGAACA TTACATGAGT
ATAAGGCGAT AGGTCTCAC 2040 GTAGCTGTG CAAAGAAACT AGCTGCTAAA GAGTTAAA TAAAGCCAGG AATGTAATT 2100

GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA
GAATATTACA TGGAGAACCA GGTCTTCCA 2220 GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG
2280 ACAGACAAG TCGGCTTAC TTCCTGGCTT AACATTAAAA AATCC //
// TGA 2328

PFU DNA POLYMERASE (V93 R OR E) - (PCNA) fusion protein (Fig. 17-Z)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGATTA CATACTGAA GAAGGAAAC CTGTTATTAG GCTATTCAA 60 AAAGAGAACG GAAATTAA GATAGACAT
GATAGAACCTT TTAGACCATA CATTACGCT 120 CTCTCAGGG ATGATTCAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGCATGGA 180
AAGATTGTGA GAATTGTGA TGTAGAGAAG GTTGAGAAA AGTTCTCGG CAAGCCTATT 240 ACCGTGTGA AACTTTATT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
CTCATCGACA AAGGCTTAAT ACCAATGGAG GGGGAAGAAG AGCTAAGAT TCTGCTTC 420 GATATAGAAA CCTCTATCA CGAAGAGAA
GAGTTTGAA AAGGCCCAAT TATAATGATT 480 AGTTATGAG ATGAATATGA AGCAAAGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTG TATCAAGCGA GAGAGAGATG ATAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTTCC ATATTAGCG 660 AAAAGGGCAG AAAAAGCTGG GATTAAATTA ACCATTGGAA GAGATGGAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGCTGTA GAAGTCAAG GAAGATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTG GAAAGCCAAA GGAGAAGTA TACGCCGACG AGATAGCAA AGCTGGGAA 900
AGTGAGAGA ACCTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GCGAATTAT 960 GAAGTGGGA AAGAAATCCT TCCAATGGA
ATTGAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTCAAGGTC AAGCACAGGG AACCTGTAG AGTGTTCTT ACTTAGGAAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAC AAGCCAAGTG AAGAGAGTA TCAAAGAAAG 1140 CTCAGGAGA GCTACACAGG
TGGATTCGTT AAAGAGCCAG AAAAGGGGT GTGGGAAAC 1200 ATAGTATACC TAGATTTAG AGCCCTATAT CCTCGATTA TAATTACCA
CAATGTTCT 1260 CCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGCA
AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGA ACTCAAGATC
CTATAGAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAATTTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTAAGAGCGT GGAAGAAAG 1560 TACATCGAGT TAGTATGGA GGAGCTCGAA
GAAAGTTG GATTAAAGT CCTTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCA GGAGGAGAA GTGAGGAAAT AAAGAAAAAG
1680 GCTCTAGAAT TTGTAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTGAATAT 1740 GAAGGTTTT ATAAGAGGG
ATTCTTCGTT ACGAAGAAGA GGTATCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG
TGAATTGCA 1860 AAAGAACTC AAGCTAGAGT TTGAGAGACA ATACTAAAAC ACGGAGATGT TGAAGAGCT 1920 GTGAGAATAG
TAAAGAAAGT AATACAAAAG CTGCGCAATT ATGAATTC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT
ATAAGCGAT AGGCTCTCAC 2040 GTAGCTGTTG CAAAGAACT AGCTGTAAG GAGTTAAA TAAAGCCAGG AATGTAATT 2100
GGATACATAG TACTTAGAGG CGATGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA

28/5/82

GAATATTACA TGGAGAACCA GGTCTTCCA 2220 GCGGTACTTA GGATATTGA GGGATTGGA TACAGAAGG AAGACCTCAG ATACCAAAG
 2280 ACAAGACAAG TCGGCTAAC TTCCTGGCTT AACATTAAA AATCC // 2328
 ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
 ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
 AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
 TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
 ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
 CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
 AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
 GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
 GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
 GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
 CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
 TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
 GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
 GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

PFU DNA POLYMERASE (G387P/V93R OR E)-(PCNA) fusion protein (Fig. 17-AA)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGATTA CATACTGAA GAAGGAAAC CTGTATTAG GCTATTCAAA 60 AAAGAGAAG GAAATTTAA GATAGAGCAT
 GATAGACTT TTAGACCATTA CATTACGCT 120 CTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGGCATGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTCTCGG CAAGCCTATT 240 ACCGTGTGA AACTTTATTT GGAACATCCC
 CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
 CTCATCGACA AAGCCCTAAT ACCAATGGAG GGGAGAAG AGCTAAGAT TCTGCCCTTC 420 GATATAGAAA CCCTCTATCA CGAAGAGAA
 GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAATGA AGCAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
 GTTGAGGTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGAT TATCAGGAG 600 AAGATCCTG ACATTATAGT TACTTATAAT
 GGAGACTCAT TCGCATTCCC ATATTAGCG 660 AAAAGGCGAG AAAAAGCTGG GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGGCGATAT GACGCTGTA GAAGTCAAGG GAAGATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAATCTC
 CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTG GAAAGCCAAG GAGAGAGTA TACGCCGACG AGATAGCAAA AGCCTGGGA 900
 AGTGAGAGA ACCTTGAGAG AGTGCCAAA TACTCGATGG AAGATGCAAA GGCACTTAT 960 GAACTGGGA AAGAATCCT TCCAATGAA
 ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGATG TTTCAAGGTC AAGCACAGGG AACCTGTAG AGTGTTCTT ACTTAGGAAA

1080 GCCTACGAAA GAAACGAAGT AGCTCCAAC AAGCCAAGTG AAGAGGAGTA TCAAGAAGG 1140 CTCAGGAGA GCTACACACC
 NGGATTCGTT AAAGAGCCAG AAAAGGGTT GTGGAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCTCGATT TAATTACCA
 CAATGTTCT 1260 CCCGATCTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGA
 AGGACATCCC TGGTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGA 1380 AGACAAAGA TTAAGACAAA AATGAAGGA ACTCAAGATC
 CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAATTTCTT TCTACGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGCTACTG TAAGGAGTGT GCTGAGAGCG TTAGTGCTTG GGAAGAAAG 1560 TACATCGAGT TAGTATGGA GGAGCTCGAA
 GAAAGTTTG GATTAAAGT CCTTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAT AAAGAAAAAG
 1680 GCTCTAGAAT TTGTAAAAA CATAATTCA AAGCTCCCTG GACTGCTAGA GCTGAATAT 1740 GAAGGTTT ATAAGAGGG
 ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGA 1800 GAAGGAAAG TCATTACTCG TGGTTAGAG ATAGTTAGGA GAGATTGAG
 TGAATTTGA 1860 AAAGAACTC AAGCTAGAGT TTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920 GTGAGAATAG
 TAAAGAAGT AATACAAAAG CTGGCCAATT ATGAATTCC ACGAGAGAAG 1980 CTGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT
 ATAAGCGGAT AGTCTCTAC 2040 GTAGCTGTG CAAAGAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGTAATT 2100
 GGATACATAG TACTTAGAG CGATGCTCCA ATTAGCAATA GGCAATTCT AGCTGAGGA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA
 GAATATTACA TGGAGACCA GGTCTTCCA 2220 GCGTACTTA GAATATTGA GGGATTGGA TACAGAAAGG AAGACTCAG ATACCAAAG
 2280 ACAAGACAAG TCGCCTAAC TTCCTGCTT AACATTAAA AATCC // 2328

// ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
 ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
 AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
 TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
 ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
 CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
 AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
 GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
 GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
 GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
 CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
 TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
 GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
 GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

(PCNA) - pFV DNA POLYMERASE (G387P/V93R OR E) fusion protein (Fig. 17-BB)

Fig. 17 B3 (Cont)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC .	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //	

//ATGATTTTAG ATGTGGATT CATACTGAA GAAGGAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAAGC GAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTACGCT 120 CTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGCATGGA 180
AAGATTGTGA GAATTGTGA TGTAGAGAAG GTTGAGAAA AGTTCTCGG CAAGCCTATT 240 ACCGTGTGA AACTTTATT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAATATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTGCG AAAGAGATAC 360
CTCATCGACA AAGGCCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAGAT TCTGCTTC 420 GATATAGAAA CCTCTATCA CGAAGGAGAA
GAGTTTGAA AAGGCCCAAT TATAATGATT 480 AGTTATGAG ATGAATGA AGCAAGGTG ATTACTTGA AAAACATAGA TCTTCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTCCT ATATTAGCG 660 AAAAGGGCAG AAAAATCTGG GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGCGATAT GACGGCTGTA GAAGTCAAGG GAAGATACA TTTCAGCTG 780 TATCATGTA TAACAAGGAC AATAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTG GAAAGCCAAG GGAGAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGA 900
AGTGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GCAACTTAT 960 GAATCGGGA AAGAATTCCT TCCAATGGA
ATTGAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGATG TTCAAGGTC AAGCACAGG AACCTTGTAG AGTGTTCTT ACTTAGAAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAC AAGCCAAGT AAGAGAGTA TCAAGAGG 1140 CTCAGGAGA GCTACACAC
NGGATTCGTT AAAGAGCCAG AAAAGGGTT GTGGAAAAC 1200 ATAGTATACC TAGATTTAG AGCCTATAT CCCTGATTA TAATTACCA
CAATGTTCT 1260 CCCGATACTC TAAATCTGA GGGATGCAAG AACTATGATA TCGCTCTCA AGTAGGCCAC 1320 AAGTCTGCA
AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGA ACTCAAGATC

CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAACTCTTA GCAAATCTT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGTACTG TAAGAGTGT GCTGAGAGCG TTACTGCCCTG GGAAGAAAG 1560 TACATCGAGT TAGTATGAA GGAGCTCGAA
 GAAAAGTTTG GATTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAT AAAGAAAAAG
 1680 GCTCTAGAAAT TTGTAATAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGTTTT ATAGAGGGG
 ATTCTTCGTT ACCAAGAAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAAG TCATTACTCG TGGTTAGAG ATAGTTAGGA GAGATTGGAG
 TGAATTTGCA 1860 AAAGAACTC AAGCTAGAGT TTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920 GTGAGAATAG
 TAAAGAGAGT AATACAAAAG CTGCCAATT ATGAATTC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT
 ATAAGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAGAAACT AGCTGCTAA GGAGTTAAAA TAAAGCCAGG AATGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGA 2160 TACGATCCCA AAAAGCACAA GTATGACGA
 GAATATTACA TGGAGAACCA GGTCTTCCA 2220 GCGTACTTA GATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG
 2280 ACAAGACAAAG TCGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //TAG 2328

(PCNA) - PFU DNA POLYMERASE (D141A/E143A/V93R OR E) fusion protein (Fig. 17-CC)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //	

//ATGATTTAG ATGTGATTA CATTAAGTGA GAAGGAAAC CTGTTATTAG GCTATTCAA 60 AAAGAGAACG GAAATTTAA GATAGAGCAT
 GATAGAACTT TTAGACCATA CATTACGCT 120 CTTCTCAGGG ATGATTCAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGCATGGA 180

AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240 ACCGTGTGGA AACTTTATTT GGAACATCCC
 CAAGATYXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
 CTCATCGACA AAGCCCTAAT ACCAATGGAG GGGAGAAGAG AGCTAAGAT TCTTGCCCTC 420 GCNATAGCNA CCCCTATCA CGAAGAGAA
 GAGTTTGCAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAAG ATGAATATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
 GTTGAGGTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
 GGAGACTCAT TCCGATTCCC ATATTAGCG 660 AAAAGGCGAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGCGCATAT GACGCTGTA GAAGTCAAGG GAAGATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
 CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTG GAAAGCCCAA GGAGAAGGTA TACGCCGACG AGATAGCAA AGCCTGGGA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GCAACTTAT 960 GAAGTGGGA AAGAATTCCT TCCAATGGA
 ATTACGCTT CAAGATTAGT TGGACACCT 1020 TTATGGATG TTCAAGGTC AAGCACAGG AACCTGTAG AGTGGTCTT ACTTAGGAAA
 1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGT AGAGAGATA TCAAGAAGG 1140 CTCAGGAGA
 GCTACACAGG TGGATTGCTT AAAGAGCCAG AAAGGGGT GTGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTGATTA
 TAATTACCCA CAATGTTCT 1260 CCCGATCTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGA
 ACTCAAGATC CTATAGAAA AATACTCCT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAATTTCT TCTACGGATA TTATGGCTAT
 1500 GCAAAAAGCAA GATGTACTG TAAGAGTGT GCTGAGAGCG TTACTGCCCT GGAAGAAAAG 1560 TACATCGAGT TAGTATGGA
 GGAGCTCGAA GAAAGTTTG GATTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGAGAAA GTGAGGAAT
 AAAGAAAAAG 1680 GCTCTAGAA TTGTAAATA CATAAATCA AAGCTCCCTG GACTGCTAGA CCTGAATAT 1740 GAAGGTTTT
 ATAGAGGGG ATTCTTCTT ACGAAGAAGA GGTATCAGT AATAGATGA 1800 GAAGAAAAAG TCATTACTCG TGGTTAGAG ATAGTTAGA
 GAGATTGGAG TGAATTGCA 1860 AAAGAACTC AAGCTAGAGT TTGGAGACA ATACTAAAAC ACGAGATGT TGAAGAAGCT 1920
 GTGAGAATAG TAAAGAAGT AATACAAAAG CTGCAATT ATGAATTC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAGACCA
 TTACATGAGT ATAGGCGAT AGGTCCTCAC 2040 GTAGCTGTG CAAGAAAAGT AGCTGCTAAA GAGTTAAAA TAAAGCCAGG AATGTAATT
 2100 GGATACATAG TACTTAGAG CGATGCTCA ATTAGCAATA GGGCAATTCT AGCTGAGGA 2160 TACGATCCCA AAAAGCACAA
 GTATGACGCA GAATATTACA TGGAGAACA GTTCTTCCA 2220 GCGTACTTA GATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG
 ATACCAAAG 2280 ACAAGACAAG TCGGCTAAC TTCCTGCTT AACATTAAAA AATCC // 2328

TGA

PFU DNA POLYMERASE (D141A/E143A/V93R OR E) - (PCNA) fusion protein (Fig. 17-DD)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTATG ATGTGATTA CATACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAATTTAA GATAGAGCAT
 GATAGAACTT TTAGACCATA CATTACGCT 120 CTTCACAGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGGA AAGCATGGA 180

Fig. 17 DD (cont)

AAGATTGTGA GAATTGTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCGG CAAGCCTATT 240 ACCGTGTGGA AACTTTATT GGAACATCCC
CAAGATYXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
CTCATCGACA AAGCCCTAAT ACCAATGGAG GGGAGAAGAG AGCTAAGAT TCTTGCCCTC 420 GCNATAGCNA CCCCTATCA CGAAGAGAA
GAGTTTGAA AAGGCCCAAT TATAATGATT 480 AGTTATGACG ATGAATATGA AGCAAGGTG ATTACTTGA AAACATAGA TCTTCCATAC 540
GTTGAGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTTCC ATATTTAGCG 660 AAAAGGCGAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGCGGATAT GACGCTGTA GAAGTCAAGG GAAGATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTG GAAAGCCCAA GGAGAAGTA TACGCCGACG AGATAGCAAA AGCCTGGAA 900
AGTGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GCGCACTTAT 960 GAAGTCGGGA AAGAATTCCT TCCAATGGAA
ATTGAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAC AAGCCAAGTG AAGAGAGTA TCAAGAAGG 1140 CTCAGGAGA
GCTACACAGG.TGGATTGCTT AAAGAGCCAG AAAGGGGTT GTGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCTCGATT
TAATTACCCA CAATGTTCT 1260 CCCGATCTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTCTGCA AGGACATCCC TGTTTATA CCAAGTCTCT TGGACATTT GTTAGAGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGAA
ACTCAAGATC CTATAGAAA AATACTCCT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAATCTT TCTACGGATA TTATGGCTAT
1500 GCAAAAAGCAA GATGCTACTG TAAGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAAAG 1560 TACATCGAGT TAGTATGAA
GGAGCTCGAA GAAAAGTTG GATTAAAGT CCTCTACATT 1620 GACACTGATG GTCTTATGC AACTATCCCA GGAGAGAAA GTGAGGAAAT
AAAGAAAAG 1680 GCTCTAGAAT TTGTAAATA CATTAATCA AAGCTCCCTG GACTGCTAGA GCTGAATAT 1740 GAAGGTTTT
ATAAGAGGG ATTCTTCTT ACGAAGAAGA GGTATGAGT AATAGATGAA 1800 GAAGAAAAG TCATTACTCG TGGTTAGAG ATAGTTAGGA
GAGATTGGAG TGAATTTGCA 1860 AAAGAACTC AAGCTAGAGT TTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAGT AATACAAGA CTTGCCAATT ATGAATTC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAGACCA
TTACATGAGT ATAAGCGAT AGTCTCTAC 2040 GTAGCTGTG CAAAGAACT AGCTGTAAA GGAGTTAAA TAAAGCCAGG AATGTAATT
2100 GGATACATAG TACTTAGAG CGATGCTCA ATTAGCAATA GGGCAATCT AGCTGAGAA 2160 TACGATCCCA AAAAGCACAA
GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220 GCGGTACTTA GGATATTGA GGGATTGGA TACAGAAAGG AAGACCTCAG
ATACCAAAG 2280 ACAAGACAAG TCGGCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

// ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648

25/86

GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

KOD DNA POLYMERASE - (PCNA) fusion protein (Fig. 17-EE)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTCG ACGACTGACTA CATAACCGAG GATGGAAGC CTGTCAATAG AATTTCAAG 60
AAGGAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCTTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAAGTT 240
GAGGCTTGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATPAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGATTAGT GCCAATGAA GCGGACGAGG AGCTGAAAT GCTCGCCTTC 420
GACATTGAAA CTCTTACCA TGAGGCGGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCC ACGAGGAAG GCGCAGGGTG ATAACCTTGA AGAACGTGA TCTCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGAGATG ATAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCCG ACGTCTCAT AACCTACAAC GCGGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTGAGAGGA TGGGCGACAG GTTGGCCGTC GAAGTGAAG GACGGATACA CTTGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTATGAA 840
GCCGCTCTCG GTCAGCCGAA GGAGAAGTT TACGCTGAGG AAATAACCAAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCCG TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCTT TCCGATGAG GCGCAGCTTT CTGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCATGAGA GGAATGAGCT GGGCCCCGAAC AAGCCCCGATG AAAAGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAA GAGCCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTAGATC CCTGTACCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGAGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAAGCCACG ATTGACCCGA TCGAGAAGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGA GAGAGCGTAA CGGCCCTGGG AAGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740

GGCTTCTACA AACCGGCTT CTTCGTACCG AAGAAGAAT ATGCGTGAT AGACGAGGAA 1800
 GGCAAGATTA CAACCGCCGG ACTTGAGATT GTGAGCCGTG ACTGAGCGGA GATAGCGAAA 1860
 GAGACGCAGG CGAGGTTCT TGAAGCTTTG CTAAGGACG GTGACGTGGA GAAGCCGTG 1920
 AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGTTCCGCC GGAGAAGCTG 1980
 GTGATCCACG AGCAGATAAC GAGGATTTA AAGACTACA AGGCAACCGG TCCCCACGTT 2040
 GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAATAC GCCCTGGAAC GGTGATAAGC 2100
 TACATCGTGC TCAAGGGCTC TGGGAGGATA GCGACACAGG CGATACCCTT CGACGAGTTC 2160
 GACCCGACGA AGCACAAGTA CGACCCGAG TACTACATTG AGAACCAAGT TCTCCAGCC 2220
 GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
 AGACAGGTTG GTTGAGTGC TTGGCTGAAG CCGAAGGAA CT 2325

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
 ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
 AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
 TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
 ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
 CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
 AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
 GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT GGA GAA GTC CTA AAA GAT GCT 432
 GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
 GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
 CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
 TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
 GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
 GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

(PCNA) - KOD DNA POLYMERASE fusion protein (Fig. 17-FH)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
 ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
 AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
 TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
 ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
 CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324

Fig.17 FF (con't)

AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //	

```
//ATGATCCTCG ACACTGACTA CATACCAG GATGGAAGC CTGTCTAAG AATTCAAG 60
AAGGAAACG GCGAGTTAA GATTGAGTAC GACCGACTT TTGAACCTA CTTCTACGCC 120
CTCCTGAAG ACCATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAGAAG GTTCAGAAGA AGTCCCTCG GAGACCAGTT 240
GAGTCTTGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGATTAGT GCCAATGGAA GCGCAGCAGG AGCTGAATAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GCGCAGGGTG ATAACCTTGA AGAACGTGA TCTCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGCGACAGG GTTGCCTGC GAAGTGAAG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACCGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCCTCG GTCAGCCGAA GGAGAAGTT TACGCTGAGG AAATAACCA AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTACATAC 960
GAGCTTGGGA AGGAGTTCTT TCCGATGAGG GCCCAGCTTT CTGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCTT CCTCAGGAAG 1080
GCCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GAGTGTGCA GAGAGCGTAA CGGCTGGGG AAGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
```

GGCTTCTACA AACCGGCTT CTTCGTACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAGATATA CACGCGCGG ACTTGAGATT GTGAGCGGTG ACTGAGCGGA GATAGCGAAA 1860
GAGACGCAGG CGAGGTTCT TGAAGCTTTG CTAAGAGACG GTGACGTGGA GAAGCGCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGATTTA AAGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GCGGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACCGCGAG TACTACATTG AGAACCAAGT TCTCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTGAAGTGC TTGGCTGAAG CCGAAGGGA CT //TAG 2325

(PCNA) -Vent DNA POLYMERASE FUSION PROTEIN (Fig. 17-GG)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT CAA GAG GAG ACA AAG ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //

ATGATACTGG ACACTGATT CATAACAATA GATGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTAA AATAGAATT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAG ATGACTCCGC TATGAGGAG ATAAAGGCAA TAAAGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGTCTGA TGCAGTGAAG GTCAGGAATA AATTTTGGG AAGGAAGTT 240

GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGCGTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTGGAA AGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGGCAGAGTA ATCACATGGA AAAATATCGA TTGGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAATG ATAAGCGTT TTGTTCAAGT TGTAAAGAA 600
AAAGACCCCG ATGTGATTAAT AACTTACAAT GGGGACAATT TTGATTGGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTT GTGTGGAAT TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTCCG AAGGACGATA AACCTCCCA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACCTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACCTA CCTGGGAGGA TATGTAAGAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAAATG AAATCCACAA TTGACCCGAT CGAAAAAGAA 1440
ATGCTCGATT ATAGGCAAG GGCATATTAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGTTCTT 1620
TATCGCGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCCTGA ACTCATTA 1680
AAGAAAGCCA AGGAATTCTT AAACCTACATA AACTCCAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTGA GAGGCTATAC TTAAAGAGGG AAGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAAATAG CAAAATACAG GGTTCACCTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCC CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATTA GCGATAGGCT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTGATATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

V_{ent} DNA POLYMERASE - (PCNA) FUSION PROTEIN (Fig. 17-HH)

Fig. 17HH (cont)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACACTGATTA CATAACAATA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAAGCTT GACCCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAGGCCAA TAAAGGGCGA GAGACATGGA 180
AAAACGTGTA GAGTGCTCGA TGCAGTGAAA GTCAGGAATA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCTTT 420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTTGGA AGGCCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGGCAGAGTA ATCACATGGA AAAATATCGA TTGCGCGTAT 540
GTCCATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTGGC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTGGGCTT GTCTTAGGAA GGGACAAGA ACATCCCGAA 720
CCCAAGATTG AGAGGATGGG TGATAGTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGCA 960
ACGTATGAGC TCGGAAGGA ATTCTTCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGAGTG GTATCTTTTA 1080
AGGTTGGCAT ACGCGAGGA TGAACCTTGA CCGAACAAC CTGATGAGGA AGAGTATATA 1140
CGGCGCTTAA GAACAACCTA CCTGGGAGGA TATGTAAGA AGCCAGAAAA AGGTTGTGG 1200
GAAAAATATCA TTTATTGGA TTTCGCGAGT CTGTACCCTT CAATAATAGT TACTCACAC 1260
GTATCCCCAG ATACCCCTGA AAAAGAGGCG TGTAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGT TCTGCAAGGA CTTTCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAAATG AAATCCACAA TTGACCCGAT CGAAAAAGAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTGCGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTA 1680
AAGAAAGCCA AGGAATTCCT AAACCTACATA AACTCCAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTGATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGAGTGAG 1860

ATAGCTAAGG AGACTCAGGC AAAGGTTTGA GAGGCTATAC TTAAGAGGG AAGTGTGAA 1920
 AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAATAG CAAAATACAG GGTCCACTT 1980
 GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTTA AGGACTACAA AGCCATTGGC 2040
 CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGA TAAAGTGAA ACCGGCACA 2100
 ATATTAAGCT ATATCGTCT CAAAGGAGC GGAAGATTA CCGATTAGGT AATTTTACTT 2160
 ACAGATAAGC ATCCTAGAAA ACACAAGTAC GATCCGACT ACTACATAGA AAACCAAGTT 2220
 TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
 CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
 ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
 AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
 TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
 ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
 CTC AAG AAA -GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
 AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
 GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
 GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
 GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
 CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
 TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
 GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
 GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

Deep Vent- (PCNA) DNA polymerase fusion protein (Fig. 17-II)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG ACGCTGACTA CATCACCAGG GATGGGAGC CGATTATAAG GATTTCAAG 60
 AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAACT TTAGACCTTA CATTACGCT 120
 CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCA GAGGCATGG 180
 AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT 240
 GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
 AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCCG GAAGAGGTAC 360

Fig. 17 II (cont)

CTAATAGACA AAGCCTAAT TCCAATGGA GGCATGAAG AGCTCAAGTT GCTCGCATTT 420
GACATAGAAA CCCTCTATCA CGAAGGGAG GAGTTGCGA AGGGCCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATACCTGGA AAAAGATCGA TCTCCCGTAC 540
GTCGAGGTAG TTTCACGCGA GAGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGAG 600
AAAGATCCCG ATGTTATAAT TACCTACAAC GCGGATTTCT TCGACCTTCC CTATCTAGTT 660
AAGAGGCGCG AAAAGCTCG GATAAAGCTA CCCCTGGGA GGGACGGTAG TGAGCCAAAG 720
ATGCAGAGGC TTGGGATAT GACAGCGGTG GAGATAAAG GAAGATACA CTTGACCTC 780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCTCGAGGC AGTTTATGAG 840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCAG AGATAGCTGA GGCTGGAG 900
ACTGGAAGG GACTGAGAG AGTTGCAAG TATTCAATGG AGGATGCAAA GGTAACGTAC 960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTT CAAGTTAGT CGGCCAGCCC 1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTG AGTGTACCT CCTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGATG AGAGGAGTA CGAGAGAAGG 1140
CTAAGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCG AGAAAGGCT CTGGAGGGG 1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCTCGATTA TAATCACCA TAACGTCTCA 1260
CCGATACGC TGAACAGGGA AGGCTGTAG GAATACGATG TCGCCCCAGA GGTGGGCAC 1320
AAGTTCTGCA AGGACTTCCC GGGGTTATC CCCAGCCTGC TCAAGAGGTT ATTGATGAA 1380
AGGCAAGAAA TAAAGAGGA GATGAAGCT TCTAAGACC CAATCGAGAA GAAGATGCTT 1440
GATTACAGGC AACGGCAAT CAAATCCTG GCAACAGCT ATTATGGTA TTATGGTAC 1500
GCAAAAGCCC GTTGTAAGT TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGAGGAA 1560
TATATAGAGT TCGTAAGGAA GGAAGTGGAG GAAGAGTTG GGTCAAGT CTTATACATA 1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGAGAT AAAGAAGAAA 1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCAG GGCTGTTGA GCTTGAATAC 1740
GAGGCTTCT ACGTAGAGG GTTCTTCGTG ACGAAGAGA AGTATGCGT GATAGATGAG 1800
GAAGGGAAGA TAACTACTAG GGGGCTTGA ATAGTCAGGA GGACTGGAG CGAATAGCC 1860
AAAGAAACCC AAGCAAAAGT CCTAGAGCT ATCCTAAGC ATGGCAACGT TGAGGAGGCA 1920
GTAAGATAG TTAAGAGGT AACTGAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG 1980
CTAGTTAATT ACGAGCAGAT CACGAGGCC CTTACAGAGT ACAAGGCTAT AGGTCCGCAC 2040
GTTGCCGTGG CAAAAGGTT AGCCGCTAGA GGAGTAAGG TGAGGCTGG CATGGTGATA 2100
GGGTACATAG TGCTGAGGG AGACGGGCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCTTTGGG TACAGGAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGCTTAC GGCATGGCTT AACATCAAGA AGAAG // 2328

// ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216

ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC-TTA ATA 270
 CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
 AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
 GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
 GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
 GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
 CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
 TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
 GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
 GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

(PCNA) - Deep Vent DNA polymerase fusion protein (Fig. 17-J)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
 ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
 AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
 TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
 ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
 CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
 AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
 GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
 GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
 GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
 CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
 TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
 GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
 GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //

//ATGATACTTG ACGCTGACTA CATCACCAGG GATGGGAAGC CGATTATAAG GATTTCGAAG 60
 AAAGAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTACGCT 120

104/86

Fig 17JJ (Cont)

CTCCTCAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG	180
AAGATAGTGA GAATTATAGA TGCCGAAAG GTAAGGAAGA AGTTCCTGGG GAGCCGATT	240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGAC XXX C CCGCAATAAG GGATAAGATA	300
AGAGAGCAAT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCCG GAAGAGGTAC	360
CTAATAGACA AAGCCCTAAT TCCAATGGAA GCGCATGAAG AGCTCAAGTT GCTCGCATTT	420
GACATAGAAA CCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGCCCAT TATAATGATA	480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGA AAAGATCGA TCTCCCGTAC	540
GTCGAGGTAG TTCCACGCGA GAGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGAG	600
AAAGATCCCG ATGTTATAAT TACCTACAAC GCGATTCTT TCGACCTTCC CTATCTAGTT	660
AAGAGGCCCG AAAAGCTCCG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG	720
ATGCAGAGGC TTGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTGACCTC	780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCTCGAGGC AGTTATGAG	840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCAGC AGATAGCTGA GGCCCTGGAG	900
ACTGGAAGG GACTGGAGAG AGTTGCAAG TATTCAATGG AGGATGCAAA GGTAAACGTAC	960
GAGCTCGGTA GGGAGTCTT CCCAATGGAG GCCCAGCTT CAAGTTAGT CGGCCAGCCC	1020
CTGTGGGATG TTTCTAGTTC TTCAACTGGC AACTTGGTGG AGTGTTACCT CCTCAGGAAG	1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGAGTA CGAGAGAAGG	1140
CTAAGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGCT CTGGAGGGG	1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCTCGATTA TAATCACCCA TAACGTCTCA	1260
CCGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTGGGCAC	1320
AAGTTCTGCA AGGACTTCCC GGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGATGAA	1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT	1440
GATTACAGGC AACGGGCAAT CAAAACTCTG GCAAAACAGCT ATTATGGTA TTATGGTAC	1500
GCAAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGAGGGAA	1560
TATATTAGAGT TCGTAAGGAA GGAACCTGAG GAAAGTTCCG GGTCAAAGT CTTATACATA	1620
GACACAGATG GACTCTACGC CACAATTCTT GGGCAAAAC CCGAGGAGAT AAAGAAGAAA	1680
GCCCTAGAGT TCGTAGATTA TATAACGCC AAGCTCCAG GGCTGTTGA GCTTGAGTAC	1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG	1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC	1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA	1920
GTAAGATAG TTAAGGAGGT AACTGAAAG CTGAGCAAGT ACGAATATACC TCCAGAAAG	1980
CTAGTTATT ACGAGCAGAT CACGAGGCC CTTACAGAGT ACAAGGCTAT AGTCCGCAC	2040
GTTGCCGTGG CAAAAAGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCCTG CATGGTGATA	2100
GGGTACATAG TGCTGAGGG AGACGGGCCA ATAAAGCAAGA GGGCTATCTT TGCAGAGGAG	2160
TTGATCTCA GGAAGCATTA GTATGACGCT GAGTATTACA TAGAAATCA GGTTTTACCCT	2220
GCCGTTCTTA GAATATTAGA GGCCTTTGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG	2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA	2328

JDF-3 - (PCNA) fusion protein (Fig. 17-KK)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACC GGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCT
ACGGCTCCTCAGGGACGACTCTGCCATCGAAGAATCAAAAAGATAACCGGAGAGCGACGGCAGGGTCTTAAGTTAAGCGCGCGGAGAAGGTGAAGAAAAGTTCCCTCGG
CAGGTCTGTGAGGCTGGTCTCTACTTCACCGCACCCCGCAGGACXXXCCCGCAATCCCGACAAATAAGGAAGCACCCCGGTCATCGACATCTACGAGTACGACATACCC
TTGCGCAAGCGCTACCTCATAGACAAAGGCCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAACTCATGTCTTGGACATCGAGACGCTTACCAAGGAGAAGATTGGAA
CCGGCCGATTCTGATGATAAGCTACCGCCGATGAAGCGAGCGCGCGTGATATACTGGAAGAAGATCGACCTTCCCTTACGTTGAGGTGTCTCCACCGAGAAGAGATGATTAA
GGCCTTCTTGAGGTCGTTAAGGAGAAGACCCCGACGTCTGTATACATACACGGCGACAATTGCACTTCCCTACCTGA AAAAGCGCTGTGAGAAGCTTGGCGTAGCTTT
ACCTCGGAGGAGCGGAGCGGAGCGGAGAAGATACAGCGCATGGGGACAGGTTTGGCGTCGAGGTGAAGGCGAGGTTACACTTTCGACCTTTATCCAGTCATAAGCGCACATAA
ACCTCCCGAACCCTACACCTTGAGGCTGTATACGAGCGGTTTTCGCAAGCCCAAGAGAAGGTTCTACGCCGAGAGATAGCCACCGCTGGGAGACCGCGGAGGGCTTGAGAG
GGTCGGCGCTACTCGATGAGGACCGGAGGTTACTTACGAGCTTGGCAGGAGTTCTTCCGATGAGGCCCAAGCTTTCAGGCTCATCGGCCAAGCCTCTGGAGCTTTC
CGCTCCAGCACCGGCAACCTCGTGAAGTGTCTCTTAAGGAAGCCCTACGAGGAACGAACTCGCTCCCAACAAGCCCCGACGAGGAGCTGGCGAAGGAGGAGGAGGCT
ACGCCGGTGGCTACGTCAGGAGCCGGAGCGGGACTGTGGACAATATCGTGTATCTAGACTTTCGTAGTCTTACCTTCAATCATATACACCACAACGTCCTCGCCAGATAC
GCTCAACCGCGAGGGGTAGAGAGCTACGACGTTGCCCCCGAGGTCCGTCACAAGTTCTGCAAGGACTTCCCGGCTTCATTCCGAGCCTGCTCGAAAACCTGCTGAGGAAAG
CAGAAGATAAAGAGGAAGATGAAGGCAACTCTGACCCGCTGAGAAGAATCTCCTCGATTACAGGCAACGCGCCATCAAGATTCTCGCCACAAGCTTACCGGCTACCGGCT
ATGCCAGGGCAAGATGCTACTGCAAGGAGTCCGCCGAGAGCGTTACGGCATGGGAAGGAGTACATCGAAATGTCATCAGAGAGCTTGAGGAAAAGTTCGGTTTAAAGTCT
CTATGACAGACACAGACGCTCTCCATGCCACCAATCTCTGAGCGGACCGCTGAACGAAATAAGTACCGCGGTATCGACGAGGAGGGAAGGCAAGATTAACCTATATCAATCCAAACTGCCGCTTCTC
GAACTCGAATACGAGGGCTTCTACGTCAGGGCTTCTTCTGTCACGAAGAATAAGTACCGCGGTATCGACGAGGAGGGAAGGCAAGATTAACCAACCGCGGCTTGAAGATGTCAGCGCG
ACTGGAGCGAGATAGCGAAGGAGACGCAAGCGGAGGTTTGGAGGCGATCTCAGGCACGGTGAAGAGCGCTCAGAATTGTCAAGGAAGTCAACCGAATAAGCTGAGCAA
GTACGAGGTTCCCGCGAGAAGCTGTTATCCACGAGCAGATTAACCGCGAGCTCAAGGACTACAAGGCCACCGCGCACAGTAGCCATAGCGAAGCGTTTGGCCGACAGAGT
GTTAAATCCGGCCCGAAGCTGTGATAAGCTACATCGTCTTGAAGGCTCCGGAAGGATAGCGACAGGCGGATTCCTTCGACGAGTTGCAACCGAAGCAAGCAAGTACGATG
CGGACTACTACATCGAGAACGAGTTCTGCCGCGAGTTGAGAGAATCTCAGGGCTTCCGCTACCGCAAGGAAGACCTGCGCTACCAAGAAGACGAGGCAAGTCCGGCTTGGCGC
GTGGCTGAAGCCGAAGGGGAAGAAGAAG//

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486

GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA	

(PCNA) - JDF-3 fusion protein (Fig. 17-LL)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //	

//ATGATCCTTGACGTTGATTACATCACCGAAGTGAAGACCCGTCATCAGGCTCTTCAAGAAGGAAACGGCAGTTTCAGGATTGAATACGACCCGAGTTCCGAG
CCCTACTTCTACCGCTCCTCAGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGGAGAGCGACGCAAGGTCTTAAGTTAAGCCGCGGAGAAAGT
GAAGAAAAAGTTCCCTCGGCAAGTCTGTGAGGTCTGGGTCTCTACTTCAACGACCCGCAAGACXXXCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGTCA
TCGACATCTACGAGTACGACATACCTTCGCCAAGCGCTACTCATAGACAAGGCCCTAATCCGATGGAAGGTGAGGAAGAGCTTAACTCATGTCTTGGATC
GAGACGCTCTACCAAGGAGGAGAGAGATTGGAACCGGGCCGATTCTGATGATAAGCTACGCCGATGAAGCGAGCGCGCGTGATACTGGAAGAAGATCGACCT
TCCTTACGTTGAGGTTGTCTCCACCAGAGAGAGATGATTAGCGCTTCTGAAGGTCTGTTAAGAGAGAGACCCGAGACGTGCTGATAACATACACGGGACAACT
TCGACTTCGCTTACCTGAAGAAAGCGCTGTGAGAAAGCTTGGCGTGAGCTTTAACCTCGGAGAGGACCGGAGCGGAGATACAGCGCATGGGGACAGGTTTGGC
GTCGAGGTGAAGGGCAGGCTACACTTCGACCTTTATCCAGTCATAGAGCGCACCATTAACCTCCGACCTACACCTTGAGGCTGTATACGAGCGGTTTTTCGCCAA
GCCCAAGGAGAGGTCTACCGCCGAGAGATAGCCACCGCTGGAGAGACCGGAGGGGCTTGAGAGGCTCGCGCTACTCGATGAGGACCGGAGGTTACTTACG
AGCTTGGCAGGAGTTCTTCCGATGAGGCCCAAGCTTTCAGGCTCATCGGCCCAAGGCTCTGGGACGTTTCCCGCTCCAGCACCGGCAACCTCGTCAGTGTTCC
CTCCTAAGGAAGGCTACGAGAGGAACGAACCTCGCTCCCAACAAGCCGACGAGAGGAGCTGGCGAGGAGAAAGGGGGGCTACGCGGTTGCTACGTCAGGAGGCC

Fig. 17 LL (cont)

GGAGCGGGA CTGTGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTAC CCTTCAATCATATACCCACAACGTCTCGCCAGATACGCTCAACCCGAGGGT
GTAGAGCTACGACGTTGCCCCGAGGTCGGTCACAAGTTCTGCAAGGACTTCCCGGCTTCATTCCGAGCCTGCTCGAAACCTGCTGAGGAAAGGCAGAAGATA
AAGAGGAAGATGAAGGCACTCTCGACCCGCTGAGAGAAGAAATCTCTCGATTACAGGCAACGCG GCGATCAAGATTCTCGCCACAAGCTACTACGGCTACTACGGCTA
TGCCAGGGCAAGATGCTACTGCAGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGAGTACATCGAAATGTCATCAGAGAGCTTGAGGAAAGTTGGTTT
AAGTCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGAGCGGACGCTGAACAAGTCAAGAAAAAGCAATGGAGTTCTTAACTATATCAATCCCAA
CTGCCCCGGCTTCTCGAACTCGAATAACGAGGCTTCTACGTCAGGGCTTCTGTCACGAAGAAAAAGTACCGCGTCAATCGACGAGGAGGCAAGATAACCAACGCG
CGGCTTGAGATAGTCAGGCGGACTGGAGCGAGATAGCGAAGGAGACCGCAGCGGAGGTTTGAGGCGGATACTCAGGCAAGGTGACGTTGAAGAGCGCTCAGAA
TTGTCAAGGAAGTCAACCGAAAGCTGAGCAAGTACGAGTTCGCCGGAAGCTGTTATCCACGAGCAGATAACGCGGAGCTCAAGGACTACAAGGCCAACCGGC
CCGCACGTAGCCATAGCCGAAGCGTTTGCCCGCCAGAGGTGTTAAATCCGGGCCCGGAAGCTGTGATAAGCTACATCGTTCTGAAGGCTCCGGAAGGATAGCGCAG
GGCGATTCCCTTCGACGAGTTCGACCCGACGAAGCACAAGTACGATGCCGACTACTACATCGAGAACCAGGTTCTGCCGCAAGTTGAGAGAATCCTCAGGGCCTTCG
GCTACCGCAAGGAAGACCTGCCGCTACCAGAAGACGAGCGAAGTCCGGCTTGCGCGTGCTGA

Sac7d gene (ACCESSION No: M87569) (Fig. 17-MM)

```
M   V   K   V   K   F   K   Y   K   G   E   E   K   E   V   D   T   S   18
ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA   54

K   I   K   K   V   W   R   V   G   K   M   V   S   F   T   Y   D   D   36
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC  108

N   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L   54
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA  162

L   D   M   L   A   R   A   E   R   E   K   K   *   67
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA TAA  201
```

Sac7d-Taq DNA polymerase fusion protein (Fig. 17-NN)

```
M   V   K   V   K   F   K   Y   K   G   E   E   K   E   V   D   T   S
ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA

K   I   K   K   V   W   R   V   G   K   M   V   S   F   T   Y   D   D
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC

N   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA

L   D   M   L   A   R   A   E   R   E   K   K   //
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

G   G   G
// GGC GGC GGT
```

```
V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC
```

Fig. 17 NN (cont)

S R G E P V Q A X Y G F A K S L L K
 AGC CGG GGG GAG CCG GTG CAG GCG OTC TAC GGC TTC GCC AAG AGC CTC CTC AAG
 A L K E D G D A V I V V F D A K A P
 GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC
 S F R H E A Y G G Y K A G R A P T P
 TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCC GCG CGG GCC CCC ACC CCA
 E D F P R Q L A L I K E L V D L L G
 GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG
 L A R L E V P G Y E A D D V L A S L
 CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG
 A K K A E K E G Y E V R I L T A D K
 GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA
 D L Y Q L L S D R I H V L H P E G Y
 GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC
 L I T P A W L W E K Y G L R P D Q W
 CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG
 A D Y R A L T G D E S D N L P G V K
 GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG
 G I G E K T A R K L L E E W G S L E
 GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA
 A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG
 A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
 L P L E V D F A K R R E P D R E R L

Fig. 17 NN (cont)

CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
 L E S P K A L E E A P W P P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG CCG GAA GGG GCC
 F V G F V L S R K E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
 L A A A R G G R V H R A P E P Y K A
 CTG GCC GCC AGG AGG GGG GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
 L R D L K E A R G L L A K D L S V L
 CTC AGG GAC CTG AAG GAG GCG CGG GGT CTT CTC GCC AAA GAC CTG AGC GTT CTG
 A L R E G L G L P P G D D P M L L A
 GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
 Y L L D P S N T T P E G V A R R Y G
 TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
 G E W T E E A G E R A A L S E R L F
 GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC GGC CTT TCC GAG AGG CTC TTC
 A N L W G R L E G E E R L L W L Y R
 GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG AGG CTC CTT TGG CTT TAC CGG
 E V E R P L S A V L A H M E A T G V
 GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG
 R L D V A Y L R A L S L E V A E E I
 CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
 A R L E A E V F R L A G H P F N L N
 GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

Fig. 17 NU (cont)

S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC
 G K T E K T G K R S T S A A V L E A
 GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTG GAG GCC
 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC
 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG
 G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC ACG AGG CTA AGT
 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG
 I R R A F I A E E G W L L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT
 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC
 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC
 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC
 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC
 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC
 K V R A W I E K T L E E G R R R G Y
 AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC

V E T L F G R R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
K S V R E A A E R M A F N M P V Q G
AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
T A A D L M K L A M V K L F P R L E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
P K E R A E A V A R L A K E V M E G
CCA AAA GAG AAG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG
V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG
L S A K E G I D G R G G G G H H H H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGC CAT CAT CAT CAT
H H *
CAT CAT TAA

Tag DNA polymerase-Sac7d fusion protein (Fig. 17-00)

G G G
// GGC GGC GGT

V T S G M L P L F E P K G R V L L V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG
D G H H L A Y R T F H A L K G L T T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

Fig. 1700 (cont)

S R G E P V Q A X Y G F A K S L L K
 AGC CGG GGG GAG CCG GTG CAG GCG OTC TAC GGC TTC GCC AAG AGC CTC CTC AAG
 A L K E D G D A V I V V F D A K A P
 GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC
 S F R H E A Y G G Y K A G R A P T P
 TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC ACC CCA
 E D F P R Q L A L I K E L V D L L G
 GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG
 L A R L E V P G Y E A D D V L A S L
 CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG
 A K K A E K E G Y E V R I L T A D K
 GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA
 D L Y Q L L S D R I H V L H P E G Y
 GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC
 L I T P A W L W E K Y G L R P D Q W
 CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG
 A D Y R A L T G D E S D N L P G V K
 GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG
 G I G E K T A R K L L E E W G S L E
 GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA
 A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CCG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG
 A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
 L P L E V D F A K R R E P D R E R L

Fig. 17 00 (cont)

CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
R A F L E R L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
L E S P K A L E E A P W P P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG CCG GAA GGG GCC
F V G F V L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
L A A A R G G R V H R A P E P Y K A
CTG GCC GCC GCC AGG GGG GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
L R D L K² E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
Y L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC GGC CTT TCC GAG AGG CTC TTC
A N L W G R L E G E E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG AGG CTC CTT TGG CTT TAC CGG
E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG
R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
A R L E A. E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

115/186

Fig. 1700 (Cont)

S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC
G K T E K T G K R S T S A A V L E A
GGC AAG ACC GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTG GAG GCC
L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC
K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG
G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC^{CA} CGC TTC AAC CAG ACG GCC ACG GCC ACG GGC AGG CTA AGT
S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG
I R R A F I A E E G W L L V A L D Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT
S Q I E L R V L A H L S G D E N L I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC
R V F Q E G R D I H T E T A S W M F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC
G V P R E A V D P L M R R A A K T I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC GCG GCC AAG ACC ATC
N F G V L Y G M S A H R L S Q E L A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC
I P Y E E A Q A F I E R Y F Q S F P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC
K V R A W I E K T L E E G R R R G Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC

986/116

Fig. 1700 (cont)

V E T L F G R R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
K S V R E A A E R M A F N M P V Q G
AAG AGC GTG CGG GAG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
T A A D L M K L A M V K L F P R L E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
P K E R A A E A V A R L A K E V M E G
CCA AAA GAG AGG GCG⁺ GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG
V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG
L S A K E G I D G R G G G G H H H H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGG CAT CAT CAT
H H //
CAT CAT //
M V K V K F K Y K G E E K E V D T S
ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
K I K K V W R V G K M V S F T Y D D
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
N G K T G R G A V S E K D A P K E L
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
L D M L A R A E R E K K // *
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TAG

11/7/86

Pfu DNA Polymerase (WT)-Sac7d fusion protein (Fig. 17-PP)

//

ccctggtcct gggtccacat atatgttctt actcgccctt atgaagaatc ccccagtcgc
tctaacctgg gttatagtga caaatcttcc tcccaccacg cccaagaag ttatttctat
caactctaca cctccccctat ttctctctt atgagatttt taagtatagt tatagaagaag
gttttact ccaaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggtatc aaaaaagaga acggaaaatt
taagatagag catgatagaa cttttaagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaagggcat ggaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtctt cggcaagcct attaccgtgt ggaaccttta
tttguaacat cccaagatg tcccactat tagagaaaa gtagagaac atccagcagt
tgtggacatc ttcgaatag atatccatt tgcagaaga taccatcgc acaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcaacgaagga gaagagtttg gaaaaggccc aattataatg attagtatg cagatgaaaa
tgaagcaag gtgattact ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaagatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaagg cagaaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaatagcgga

2011/8/11

Fig 17 pp (cont)

tatgacggct gtagaagtca agggagaagt acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttgaaaagcc
aaaaggaag gtatacgccg acgagatagc aaaaagcctgg gaaagtggag agaaccctga
gagagltgcc aaatactcga tggaaagtgc aaaggaact tatgaactcg ggaagaat
cctccaatg gaaattcagc ttcaagatt agttggacaa ctttatggg atgtttcaag
gtcaagcaca gggaaccctg tagagtggt cttactag aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaagagg gatacaaga aggtcaggg agagctacac
aggtggttc gttaaagagc cagaaaaagg gtgtggaa aacatagtat acctagatt
tagagcccta tatccctcga ttataatlac ccacatgtt tctcccgata ctctaattc
tgagggtgc aagaactatg atatcgctcc tcaagtaggc cacaaagttct gcaaggacat
ccctggttt ataccagtc tcttgggaca ttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc ctgactata gacaaaaagc
gataaaactc ttagcaaat ctttctacg atatattgct tatgcaaaag caagatgta
ctgtaaggag tgtgctgaga ggccttactgc ctggggaaga aagtacatcg agttaagt
gaaggagctc gaagaaaaagt ttgatttaa agtcctctac attgacactg atgtctcta
tgcaactatc ccaggaggag aaagtgaaga aataaagaaa aaggctctag aattgtaaa
atacataaat tcaagctcc ctgactgct agagcttga tatgaagggt ttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaatt gcaaaagaaa ctcaagctag

119/186

Fig. 17P (con+)

agttttggag acaataactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccatcacatg agtataaggc gatagtcct cacgtagctg ttgcaagaa
actagctgct aaaggagta aaataaagcc aggaatgta attgataca tagtacttag
aggcgtatgt ccaatlagca ataggccaat tctagctgag gaatacgcac ccaaaaagca
caagtatgac gcagaatat acattgagaa ccaggttctt ccagcgtac ttagatatt
ggaaggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aactccctgg cttaacatla^{*}aaaaatcccta gaaaagcgat agatatcaac ttttattcct
tctaaccctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tggttaatta aaaaccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcaactcaa acgccttcgt tagaatgtg
ctatctgcac gcttctctgg ctcggaanng gaggatcat aacaacagta tcaacattct
cagagaatg agaacatca gaaacttga ctctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt
tttgctccaa gcagagccgc tccaatgcat aacacccctg ttcccgcacc caagtccgct
acaattttt cctgtatct cctaattgat aagcaagca aaggagagta gatgctacct
ttccggagat ttgttatgc tctagccaag gtttgagat ttgtaatcct ttaactctgg
aaagtataat ttcaagctcc ttctcttca tgacagatga aaaattgttt tgtctctttt
taacttttac agaataact gtctcaatt atgacaactc ttgacatttt tacttcattta

120/186

ccagggaat gttttaagt atgaatttt tcttcatag aggagnnnn nngtccttc
ctcgatttcc ttggtgtgc tccatatgat aagttccaa agtgggtgt cagacttta
gacctcaaa taccagacga caatggtgtg ctcaactcaag ccccatatgy gttgagaaaa
gtagaagcgy cactactcag atgcttcccc aggaatgaggy ttgtgtagc tcntccnga
aagattgaga tgttcttg //

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //TGA

Sac7d - Pfu DNA Polymerase (WT) fusion protein (Fig. 17-QQ)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

//
ccctggtcct ggggccacat atatgttctt actgccttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tcccaccacgy cccaagaagy ttatttctat
caactctaca cctccccctat tttctctctt atgagatttt taagtatagt tataagaag
gttttactt ccaactgag ttagtagata tgtggggagc ataatgatth tagatgtgga
ttacataact gaagaagga aacctgttat taggtatlc aaaaagaga acggaaaatt
taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgatlc

12.1/180

Fig. 17 QQ (cont)

aaagatlgaa gaagttaaga aaataacggg ggaagggcat ggaagatlg tgagaattgt
tgatgtagag aaggttgaga aaaagttct cggcaagcct ataccggtg gaaacttta
tttggaacat cccaagatg tccccactat tagagaaaaa gtagagAAC atccagcagt
tgtgacatc ttcgaatacg atatccatt tgcaagaga taccatcag acaaggcct
aataccaatg gaaggggaa aagagctaaa gattctgcc ttcgatatag aaaccctcta
tcacgaaaga gaagagttg gaaaagccc aattataatg atagttatg cagatgaaaa
tgaaagcaaa gttgattact ggaaaaaaat agatcttcca tacgttgagg ttgtatcaag
cgaagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgact cccatattta gcgaaaaagg cagaaaaaact
tgggatttaa ttaaccatlg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggagaat acatttcgac ttgtatcatg taatacaag
gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttgaaaagcc
aaaggaagaa gtatacgcg acgagatagc aaaagccctgg gaaagtggag agaaccctga
gagagttgcc aaatactcga tggaaagatgc aaaggcaact tatgaactcg ggaagaatt
ccttccaatg gaattcagc ttccaagatt agttggacaa ccttatggg atgttcaag
gtcaagcaca gggaaacctg tagagtgtt ctacttagg aaagcctacg aaagaaacga
agtagctcca aaacagccaa gtgaagagga gtatcaaga aggtcaggg agagctacac
aggtggattc gttaagagc cagaaaaagg gtgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctccgata ctctaattct

Fig. 17 BQ (cont)

tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaaagtctt gcaaggacat
ccctggtttt ataccgaagtc tcttggaaca ttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atccctataga aaaaatactc ctlgactata gacaaaaagc
gataaaactc ttagcaaatc ctttctacgg atattatgac tatgcaaaag caagatgta
ctgtaaaggag tgtgctgaga gcgttactgc ctgggggaaga aagtacatcg agttaagtatg
gaaaggagtc gaagaaaagt ttggatttaa agtcctctac attgacactg atgtctcta
tgcaactatc ccaggaggag aaagtgaaga aataaagaaa aaggctctag aattgtaaa
atacataaat tcaagctcc ctggactgct agagcttgaa tatgaaggt ttataagag
gggattcttc gtlacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggaagagattg gagtgaaat gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgagaa gctgtgagaa tagtaaaaga
agtatacaaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccatlacatg agtataaggc gatagtcct cacgtagctg ttgcaagaa
actagctgct aaaggagtta aaataaagcc aggaatggtta attgataca tagtacttag
aggcgatggt ccaattagca ataggccaat tctaagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatc acattgagaa ccaagttctt ccaagcgtaac ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatla aaaaatccta gaaagcgat agatatcaac ttttattctt
tctaaccctt ttctatgaaa gaagaactga gcaggaattta ccagttcttc cgttatttta

tgggttaatta aaaaccatg ctcttggag aatcttcgaa taaatccct aactcaggc
 ttgtctaagt gaatagaata aacaacatca ctcaattcaa acgccttcgt tagaatgtg
 ctatctgcat gcttctctg ctcggaanng gaggttcat aacaacagta tcaacattct
 cagagaattg agaaacatca gaaacttga ctctacaac atttctaact ttgcaactct
 tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa ttgcgacgac gtagatcttt
 ttgtctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct
 acaatttttt ccttgtatct cctaattgat aagcaagcca aaggagagta gatgtacct
 ttccgggagt ttgtattgc tctaagccaag gttgggatt ttgtaacct ttaactctg
 aaagtataat ttcaagctcc ttcttctca tgacagatga aaaattgttt tgtctcttt
 taacttttac agaataaact gtctcaaat atgacaactc ttgacatttt tacttcatta
 ccagggtaat gtttttaagt atgaaatttt tcttcatag aggagnnn nngtcctctc
 ctcgatttcc ttggtgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta
 gacactcaaa taccagacga caatggtgtg ctcaactcaag ccccatatg gttgagaaaa
 gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgtgtagc tcntccnga
 aagattgaga tgttcttg // TGA

Sac7d - PFU DNA POLYMERASE (V93 R OR E) fusion protein (Fig. 17-RR)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA

124/86

TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

//ATGATTTTAG ATGTGGATTA CATACTGAA GAAGGAAAC CTGTTATTAG GCTATTCAA 60 AAAGAGAAGC GAAATTTAA GATAGACAT
GATAGAAGCTT TTAGACCATA CATTACGCT 120 CTCTCAGGG ATGATTCAA GATTGAAGAA TTAACGGGGA AAGCATGGA 180
AAGATTGTGA GAATTGTGA TGTAGAGAAG GTTGAGAAA AGTTCTCGG CAAGCCTATT 240 ACCGTGTGA AACTTTATTT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCTTAAT ACCAATGGAG GGGAGAAG AGCTAAGAT TCTGCCCTTC 420 GATATAGAAA CCTCTATCA CGAAGAGAAA
GAGTTTGAA AAGCCCAAT TATAATGATT 480 AGTTATGCA AGTAAATGA AGCAAGGTG ATTACTTGA AAAACATAGA TCTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTCCT ATATTAGCG 660 AAAAGGGCAG AAAAAGCTTG GATTAAATTA ACCATTGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGCGGATAT GACGCTGTA GAAGTCAAG GAAGATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTG GAAAGCCAAA GGAGAAGTA TACGCCGACG AGATAGCAA AGCCTGGGA 900
AGTGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATG AAGATGCAA GCAACTTAT 960 GAACCTGGGA AAGAATTCCT TCCAATGAA
ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGAGT TTCAAGGTC AAGCACAGG AACCTGTAG AGTGTTCTT ACTTAGAAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAC AAGCCAAGT AAGAGAGTA TCAAGAAGG 1140 CTCAGGAGA GTCACACAGG
TGGATTCGTT AAAGAGCCAG AAAAGGGTT GTGGAAAAC 1200 ATAGTATACC TAGATTTAG AGCCTATAT CCCTCGATTA TAATTACCA
CAATGTTTCT 1260 CCCGATCTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCTCA AGTAGGCCAC 1320 AAGTCTGCA
AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGA ACTCAAGATC
CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAGCGAT AAAACTCTTA GCAAATCTT TCTACGGATA TTATGGCTAT 1500
GCCAAAGCAA GATGTTACTG TAAGGAGTGT GCTGAGAGCG TTAAGGAGT TAGTATGGA GGAGCTCGAA
GAAAAGTTG GATTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCA GGAGAGAAA GTGAGGAAT AAGAAAAAG
1680 GCTCTAGAAT TTGTAATAA CATAAATCA AAGCTCCCTG GACTGCTAGA GCTGAATAT 1740 GAAGGTTTT ATAGAGGGG
ATTCTTCGTT ACGAAGAAGA GGTATGAGT AATAGATGA 1800 GAAGGAAAAG TCATTACTCG TGGTTAGAG ATAGTAGGA GAGATTGAG
TGAATTTGCA 1860 AAAGAACTC AAGCTAGAGT TTTGAGACA ATACTAAAAC ACGAGATGT TGAAGAAGCT 1920 GTGAGAATAG
TAAAAAGAGT AATACAAAAG CTGGCAATT ATGAATTC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT
ATAAGGCGAT AGTCTCTAC 2040 GTAGCTGTTG CAAAGAACT AGCTGCTAAA GAGTTAAA TAAAGCCAGG AATGTAATT 2100
GGATACATAG TACTTAGAG CGATGTTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGA 2160 TACGATCCA AAAAGCACAA GTATGACGA
GAATATTACA TGGAGAACA GGTCTTCCA 2220 GCGTACTTA GGATATTGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG
2280 ACAAGACAAG TCGGCTAAC TTCCTGGCTT AACATTAAA AATCC //
// TGA

PFU DNA POLYMERASE (V93 R OR E)-Sac7d fusion protein (Fig. 17-SS)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTAG ATGTGATTA CATACTGAA GAAGGAAAAC CTGTATTAG GCTATTCAA 60 AAAGAGAAGC GAAATTTAA GATAGACAT
GATAGAAGCTT TTAGACCATA CATTACGCT 120 CTCTCAGGG ATGATTCAA GATTGAAGAA TTAACGGGGA AAGCATGGA 180
AAGATTGTGA GAATTGTGA TGTAGAGAAG GTTGAGAAA AGTTCTCGG CAAGCCTATT 240 ACCGTGTGA AACTTTATTT GGAACATCCC

125/186

CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
 CTCATCGACA AAGGCTTAAT ACCAATGGAG GGGAGAAG AGCTAAGAT TCTTGCTTC 420 GATATAGAAA CCTCTATCA CGAAGGAGAA
 GAGTTTGAA AAGGCCAAT TATATGATT 480 AGTTATGCG AGTAATGA AGCAAGGTG ATTACTTGA AAACATAGA TCTTCCATTAC 540
 GTTGAGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
 GGAGACTCAT TCGCATTCCT ATATTAGCG 660 AAAAGGCGAG AAAAATTGG GATTAAATTA ACCATTGGAA GAGATGGAG CGAGCCCAAG 720
 ATGCAGAGAA TAGCGGATAT GACGGCTGTA GAAGTCAGG GAAGATACA TTTCGACTTG 780 TATCATGTAA TAACAGGAC AATAATCTC
 CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTG GAAGCCAAA GGAGAAGTA TACGCCGAG AGATAGCAAA AGCCTGGAA 900
 AGTGAGAGAG ACCTGAGAG AGTGGCCAAA TACTCGATGG AAGATGCAAA GGCACTTAT 960 GAACCTGGGA AAGAATTCT TCCAATGAA
 ATTACGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGATG TTCAAGGTC AGCACAGGG AACCTGTAG AGTGTTCTT ACTTAGAAA
 1080 GCCTACGAAA GAAACGAAGT AGCTCCAAC AAGCCAAGTG AAGAGAGTA TCAAGAAGG 1140 CTCAGGAGA GCTACACAGG
 TGGATTCGTT AAAGAGCCAG AAAAGGGTT GTGGAAAAC 1200 ATAGTATACC TAGATTTAG AGCCTATAT CCTCGATTA TAATTACCA
 CAATGTTTCT 1260 CCCGATCTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGA
 AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGAA ACTCAAGATC
 CTATAGAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAACTCTTA GCAAACTCTT TCTACGATA TTATGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTAAGTCTG GGAAGAAAAG 1560 TACATCGAGT TAGTATGAA GGAGCTCGAA
 GAAAAGTTG GATTAAAGT CCTCTACAT 1620 GACACTGATG GTCTCTATGC AACTATCCA GGAGAGAAA GTGAGGAAT AAAGAAAAG
 1680 GCTCTAGAAAT TTGTAAATA CATAATTCA AAGCTCCCTG GACTGCTAGA GCTGAATAT 1740 GAAGGTTTT ATAAGAGGG
 ATTCTTCGTT ACGAAGAGA GGTATGAGT AATAGATGAA 1800 GAAGAAAAG TCAATTACTG TGGTTAGAG ATAGTTAGA GAGATTGGAG
 TGAATTTGCA 1860 AAAGAACTC AAGCTAGAGT TTGGAGACA ATACTAAAAC ACGAGATGT TGAAGAAGCT 1920 GTGAGAATAG
 TAAAGAAAGT AATACAAAAG CTGCCAATT ATGAAATTCC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT
 ATAAGCGAT AGTCCCTCAC 2040 GTAGCTGTG CAAAGAACT AGCTGTAAA GGAGTTAAA TAAAGCCAG AATGTAAT 2100
 GGATACATAG TACTTAGAGG CGATGTCCA ATTAGCATA GGCAATTCT AGCTGAGAA 2160 TACGATCCA AAAAGCACAA GTATGACGA
 GAATATTACA TGGAGAACA GGTCTTCCA 2220 GCGTACTTA GGATATTGA GGAITTTGA TACAGAAAAG AAGACCTCAG ATACCAAAAG
 2280 ACAAGACAAG TCGGCTAAC TTCCTGGCTT AACATTAAA AATCC // 2328
 // ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

PFU DNA POLYMERASE (G387P/V93R OR E)-Sac7d fusion protein (Fig. 17-1T)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
 V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
 ATGATTTAG ATGTGATTA CATACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60 AAAGAGAACG GAAATTTAA GATAGAGCAT
 GATAGAACTT TTAGACCATA CATTACGCT 120 CTCTCAGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGCATGA 180
 AAGATTGTGA GAATTGTGA TGTAGAGAAG GTTGAGAAA AGTTTCTGG CAAGCTATT 240 ACCGTGTGA AACTTTATTT GGAACATCCC

126/186

CAAGATXXXC CCACATATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
 CTCATCGACA AAGGCCCTAAT ACCAATGGAG GGGAGAAGAG AGCTAAAGAT TCTTGCCCTC 420 GATATAGAAA CCCCTATCA CGAAGGAGAA
 GAGTTTGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAATGA AGCAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
 GTTGAGGTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
 GGAGACTCAT TCGCATTCCT ATATTAGCG 660 AAAAGGCGAG AAAAATTGG GATTAAATTA ACCATTGGAA GAGATGGAA GAGGCCAAG 720
 ATGCAGAGAA TAGCGGATAT GACGGCTGTA GAAGTCAAGG GAAGATACA TTTGACTTG 780 TATCATGTAA TAACAAGGAC AATAATCTC
 CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTGG GAAAGCCAAA GGAGAAGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGGAGAGA ACCTGAGAG AGTTGCCAAA TACTGATGG AAGATGCAAA GGCACTTAT 960 GAACTGGGGA AAGAAITCCT TCCAATGGAA
 ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGTTCTT ACTTAGAAA
 1080 GCCTACGAAA GAAACGAAGT AGCTCCAAC AAGCCAAGTG AAGAGAGTA TCAAGAAGG 1140 CTCAGGAGA GCTACACACC
 NGGATTCGTT AAAGAGCCAG AAAAGGGGT GTGGGAAAC 1200 ATAGTATACC TAGATTTAG AGCCCTATAT CCTCGATTA TAATTACCA
 CAATGTTCT 1260 CCCGATCTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGA
 AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC
 CTATAGAAA AATACTCCT 1440 GACTATAGAC AAAAAGCGAT AAACTCTTA GCAATTTCT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGTTACTG TAAAGAGTGT GCTGAGAGCG TTAAGTCTG GGAAGAAAG 1560 TACATCGAGT TAGTATGAA GGAGCTGAA
 GAAAAGTTG GATTAAAGT CCTTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCA GGAGGAGAA GTGAGGAAT AAAGAAAAAG
 1680 GCTCTAGAAT TTGTAATAA CATAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGTTTT ATAAGAGGG
 ATTCTTCGTT ACGAAGAGA GGTATGAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTAGAG ATAGTTAGGA GAGATTGGAG
 TGAATTCGA 1860 AAAGAACTC AAGCTAGAGT TTTGAGAGCA ATACTAAAC ACGAGATGT TGAAGAGCT 1920 GTGAGATAG
 TAAAGAGAGT AATACAAAAG CTGCAATT ATGAATTC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT
 ATAAGGCGAT AGGTCTCAC 2040 GTAGCTGTG CAAAGAACT AGCTGCTAAA GAGTTTAAA TAAAGCCAGG AATGTTAAT 2100
 GGATACATAG TACTTAGAG CGATGTCCA ATTAGCAATA GGGCAATCT AGCTGAGGAA 2160 TACGATCCA AAAAGCACAA GTATGACGCA
 GAATATTACA TGGAGAACCA GGTCTTCCA 2220 GCGTACTTA GGATATTGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG
 2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

PFU DNA POLYMERASE (G387P/V93R OR E)-Sac7d fusion protein (Fig. 17-UU)

127/86

Fig. 17 UV (cont)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTACGCT 120 CTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGCATGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAG GTTGAGAAA AGTTCTCGG CAAGCCTATT 240 ACCGTGTGA AACTTTATTT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCTTC 420 GATATAGAAA CCTCTATCA CGAAGAGAA
GAGTTGGAA AAGCCCAAT TATAATGATT 480 AGTTATGAG ATGAAAATGA AGCAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTTCC ATATTAGCG 660 AAAAGGGCAG AAAAAGTTGG GATTAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGCGGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTG GAAAGCCAAA GGAGAAGTA TACGCCGACG AGATAGCAAA AGCCTGGAA 900
AGTGAGAGAA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCACTTAT 960 GAACCTGGGA AAGAATTCTT TCCAATGGAA
ATTGAGCTTT CAAGATTAGT TGGACACCT 1020 TTATGGGATG TTTCAGGTC AAGCACAGGG AACCTTGTA AGTGGTTCTT ACTTAGGAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAC AAGCCAAGTG AAGAGGAGTA TCAAGAAGG 1140 CTCAGGAGA GCTACACACC
NGGATTCGTT AAAGAGCCAG AAAAGGGTT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCA
CAATGTTTCT 1260 CCCGATCTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCTCA AGTAGGCCAC 1320 AAGTTCTGCA
AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC
CTATAGAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAATTTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCTTG GGAAGAAG 1560 TACATCGAGT TAGTATGAA GGAGCTCGAA
GAAAAGTTG GATTAAAGT CCTCTACATT 1620 GACACTGATG GTCTTATG CAACTATCCA GGAGAGAAA GTGAAGAAAT AAAGAAAAG
1680 GCTCTAGAA TTGTAAATA CATAAATCA AAGTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGTTTT ATAAGAGGG
ATTCTTCGTT ACGAAGAAGA GGTATGAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTAGAG ATAGTTAGGA GAGATTGGAG
TGAATTTGCA 1860 AAAGAACTC AAGCTAGAGT TTGGAGACA ATACTAAAAC ACGAGATGT TGAAGAAAGT 1920 GTGAGATAG
TAAAGAAGT AATACAAAAG CTGCCAATT ATGAAATCC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT
ATAAGCGAT AGTCTCTAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGTTAAT 2100
GGATACATAG TACTTAGAG CGATGCTCA ATTAGCAATA GGGCAATTCT AGCTGAGAA 2160 TACGATCCA AAAAGCACAA GTATGACGA
GAATATTACA TGGAGAACCA GGTCTTCCA 2220 GCGTACTTA GGATATTGA GGGATTTGA TACAGAAAAG AAGACCTCAG ATACCAAAAG
2280 ACAAGACAAG TCGGCTAAC TTCCTGGCTT AACATTAAA AATCC //

2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

128/186

SAC7D-PFU DNA POLYMERASE (D141A/E143A/V93R OR E) fusion protein (Fig. 17-VV)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GGT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //
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//ATGATTTTATG ATGTGATTA CATACTGAA GAAGGAAAC CTGTTATTAG GCTATTCAA 60 AAAGAGACG GAAATTTTA GATAGACAT
GATAGAACTT TTAGACCATA CATTACGCT 120 CTCTCAGGG ATGATTCAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGCATGGA 180
AAGATTGTGA GAATTGTGA TGTAAGAGAG GTTGAGAAA AGTTCTCGG CAAGCCTATT 240 ACCGTGTGA AACTTTATT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATAGGATA TTCCATTTC AAAGAGATAC 360
CTCATCGACA AAGCCCTAAT ACCAATGGAG GGGGAAGAG AGCTAAAGAT TCTTGCCCTC 420 GCNATAGCNA CCTCTATCA CGAAGAGAA
GAGTTTGAA AAGCCCAAT TATAATGATT 480 AGTTATGAG ATGAAATGA AGCAAGGTG ATTACTTTGA AAAACATAGA TCTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAGAGAT TTCTCAGGAT TATCAGGAG 600 AAGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATCCC ATATTAGCG 660 AAAAGGCGAG AAAAAGCTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGAGAGAAA TAGGCGATAT GACGCGTGA GAAGTCAAG GAAGATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTG GAAAGCCAAA GGAAGAGGTA TACGCCGACG AGATAGCAAA AGCTGGGAA 900
AGTGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCACTTAT 960 GAACTCGGGA AAGAATTCTT TCCAATGGAA
ATTGAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGATG TTCAAGTTC AAGCACAGGG AACCTTGTAG AGTGTTCTT ACTTAGGAAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAC AAGCCAAGTG AAGAGAGTA TCAAGAAAG 1140 CTCAGGAGA
GCTACACAGG.TGGATTCGTT AAAGAGCCAG AAAAGGGTT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA
TAATTACCCA CAATGTTTCT 1260 CCCGATPACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA
ACTCAAGATC CTATAGAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAATTCTT TCTACGATA TTATGGCTAT
1500 GCAAAAGCAA GATGTTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGAAGAAAAG 1560 TACATCGAGT TAGTATGAA
GGAGCTCGAA GAAAGTTTG GATTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCA GGAGAGAAA GTGAGGAAAT
AAAGAAAAAG 1680 GCTCTAGAAT TTGTAATAA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTGAATAT 1740 GAAGGTTT
ATAAGAGGGG ATTCTTCGTT ACGAAGAGA GGTATGCAGT AATAGATGA 1800 GAAGAAAAG TCATTACTCG TGCTTTAGAG ATAGTTAGGA
GAGATTGGAG TGAATTGCA 1860 AAAGAACTC AAGCTAGAGT TTTGAGACA ATACTAAAC ACGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAAGT AATACAAAAG CTGCGCAAT ATGAATTC ACCAGAGAAG 1980 CTGCAATAT ATGAGCAGAT AACAGACCA
TTACATGAGT ATAAGCGAT AGGTCTCAC 2040 GTAGCTGTG CAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAG AATGTAATT
2100 GGATACATAG TACTTAGAGG CGATGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGA 2160 TACGATCCA AAAAGCACAA
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129/186

GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220 GCGTACTTA GGATATTGA GGGATTGGA TACAGAAAGG AAGACCTCAG
ATACCAAAG 2280 ACAAGACAAG TCGCCTAAC TTCCTGGCTT AACATTAAA AATCC // 2328

TGA

KOD DNA POLYMERASE - Sac7d fusion protein (Fig. 17-WW)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTCG ACACCTGACTA CATAACCGAG GATGGAAGC CTGTCAATAG AATTTCAG 60
AAGGAAAACG GCGAGTTTA GATTGAGTAC GACCGGACTT TTGAACCTA CTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAAGT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGATTAGT GCCAATGGAA GCGCAGCAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAATTGGA AGAACGTGA TCTCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGCACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGATACA CTTGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTGAGGC CGTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAAGTT TACGCTGAGG AAATTAACAC AGCCTGGGAA 900
ACCGCGGAGA ACCTTGAGAG AGTCGCCGC TACTCGATGG AAGATGCGAA GGTACATAC 960
GAGCTTGGGA AGGAGTTCTT TCCGATGGAG GCCCAGCTTT CTGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGTTCTT CCTCAGGAAG 1080
GCCATATGGA GGAATGAGCT GGCCCGGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAA GAGCCCGAGA GAGGTTGTG GGAGAACATA 1200
GTGTACCCTAG ATTTAGATC CCTGTACCC TCAATCATCA TCACCCACAA CGTCTGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTCA GAGAGCGTAA CGGCCTGGGG AAGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680

130/86

ATGAGTTCC TCAAGTATAT CAACGCCAAA CTTCGGGCG CGCTTGAGCT CGAGTACGAG 1740
 GGCTTCTACA AACGGGCTT CTTCGTACG AAGAAGAGT ATCGGTGAT AGACGAGGAA 1800
 GGCAAGATTA CAACGCCGG ACTTGAGAT GTGAGCGTG ACTGAGCGA GATAGCGAA 1860
 GAGACGCAGG CGAGGTTCT TGAAGCTTG CTAAGGACG GTGACGTGA GAAGCCGTG 1920
 AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGTTCCGCC GGAGAAGCTG 1980
 GTGATCCACG AGCAGATAAC GAGGATTTA AAGACTACA AGGCAACCG TCCCACGTT 2040
 GCCGTTGCCA AGAGTTGGC CGCAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
 TACATCGTGC TCAAGGCTC TGGAGGATA GCGACAGGG CGATACCCTT CGACGAGTTC 2160
 GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAAGT TCTCCAGCC 2220
 GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
 AGACAGGTTG GTTGAGTGC TTGGCTGAAG CCGAAGGAA CT 2325
 // ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

Sac7d - KOD DNA POLYMERASE fusion protein (Fig. 17-XX)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

//ATGATCCTCG ACACTGACTA CATTAACCGAG GATGGAAGC CTGTCAATAAG AATTTCAG 60
 AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGACTT TTGAACCTA CTCTACGCC 120
 CTCCTGAAGG ACGATTCTGC CATTGAGGA GTCAAGAAGA TAACCGCGA GAGCACGGG 180
 ACGGTGTA CGGTTAGCG GGTGAAAG GTTCAGAAGA AGTTCCTCG GAGACCAATT 240
 GAGGTCTGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGGATAAG GGACAAGATA 300
 CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCG CAAGCGCTAC 360
 CTCATAGACA AGGATTAGT GCCAATGGA GCGACGAG AGCTGAAAT GCTCGCCTTC 420
 GACATTGAAA CTCTTACCA TGAGGGCGAG GAGTTCGCC AGGGCCAAT CTTATGATA 480
 AGCTACGCCG ACGAGGAAG GCGCAGGGTG ATAAGTTGA AGAAGTTGA TCTCCCTAC 540
 GTTGACGTCG TCTGACGGA GAGGAGATG ATAAAGCGT TCCTCCGTGT TGTGAAGAG 600

13.1/186

AAAGACCCCG ACGTTCTCAT AACCTACAAC GGGGACAAC TCGACTTCGC CTATCTGAA 660
 AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
 ATTCAGAGGA TGGCGGACAG GTTTCGGCTC GAAGTGAAGG GACGATACA CTTGATCTC 780
 TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTATGAA 840
 GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAAC AGCCTGGGAA 900
 ACCGGCCGAG ACCTTGAGAG AGTCGCCCCG TACTCGATGG AAGATCGGAA GTTCACATAC 960
 GAGCTTGGA AGGAGTTCTT TCCGATGAG GCCCAGCTTT CTGCTTAAT CGGCCAGTCC 1020
 CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCTT CCTCAGGAAG 1080
 GCCTATGAGA GGAATGAGCT GGGCCCCGAC AAGCCCCGATG AAAAGGAGCT GGCAGAGA 1140
 CGGCAGAGCT ATGAAGGAGG CTATGTAAA GAAGCCGAGA GAGGTTGTG GGAGAACATA 1200
 GTGTACCTAG ATTTAGATC CTTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
 GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGAGT CGGCCACCGC 1320
 TTCTGCAAGG ACTTCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
 CAGAAGATTA AGAAGAAGAT GAAGGCCACG ATGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
 TACAGGCAGA GGGCCATCAA GATCCTGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
 AGGGCGCGCT GGTACTGCAA GGAGTGTCA GAGAGCGTAA CGGCTGGGG AAGGAGTAC 1560
 ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
 ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
 ATGAGATTCC TCAAGTATAT CAACGCCAAA CTTCCGGGGC CGCTTGAGCT CGAGTACGAG 1740
 GGCTTCTACA AACCGGCTT CTTCGTACG AAGAAGAAGT ATGCGTGAT AGACGAGGAA 1800
 GGCAAGATTA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGAGCGA GATAGCGAAA 1860
 GAGACGCAGG CGAGGTTCT TGAAGCTTTG CTAAGGACG GTGACGTCGA GAAGCCGCTG 1920
 AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGTTCCGCC GGAGAACTG 1980
 GTGATCCACG AGCAGATAAC GAGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
 GCCGTGCCA AGAGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
 TACATCGTGC TCAAGGCTC TGGAGGATA GGCAGACAGG CGATACCGTT CGACGAGTTC 2160
 GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACGAGT TCTCCAGCC 2220
 GTTGAGAGAA TTCTGAGAGC CTTCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
 AGACAGGTTG GTTGAAGTGC TTGGCTGAAG CCGAAGGGA CT //TAG 2325

Sac7d-Vent DNA POLYMERASE FUSION PROTEIN (Fig. 17-YY)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA

132/186

Fig 17.44 (cont)

AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

ATGATACTGG ACACTGATTA CATAACAATA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAAGC GGGAGTTAA AATAGAATT GACCCTCAT TTTAGCCCTA TATATATGCT 120
CTTCTCAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGTGGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXKXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGTT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCCTT 420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTTGAAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGGCAGAGTA ATCACAATGA AAAATATCGA TTGCGGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT⁴ AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATTA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTT GCTGTGAAA TCAAGGCTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAGAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGAAGACAG AAGAAAGCAT GAATAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGAGTG GTATCTTTTA 1080
AGGCTGCAT ACGCGAGGAA TGAACCTTGA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTGGA TTTCGCGAGT CTGTACCCTT CAATAATAGT TACTCACAAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATATA GAAGAAATG AAATCCACAA TTGACCCGAT CGAAAAAGAA 1440
ATGCTCGATT ATAGGCAAG GGTATTAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAAGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTA 1680
AAGAAAGCCA AGGAATTCTT AAATAACATA AACTCCAAAC TTCCAGGCTT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATTAAC AACAGGGGC TTGGAAGTAG TAAAGAGAGA TTGGAAGTAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTGA GAGGCTATAC TTAAGAGAGG AAGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAAATAG CAAATATACAG GGTTCACCTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTAA AGGACTACAA AGCCATTGGC 2040

133/186

CCTCATGTGCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAGTGAA ACCGGGCACA 2100
 ATAATAAGCT ATATCGTCT CAAGGGAGC GGAAGATAA GCGATAGGCT AATTCTACTT 2160
 ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
 TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTGGATACA GAAAGAGAGA TTTAAGGTAT 2280
 CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Vent DNA POLYMERASE - Sac7d FUSION PROTEIN (Fig. 17-ZZ)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACACGTGATTA CATACAAAA GATGGCAAGC CTATAATCCG AATTTTAA 60
 AAAGAGAACG GGGAGTTTAA AATAGAATT GACCTCATTT TTCAGCCCTA TATATATGCT 120
 CTCTCAAG ATGACTCCGC TATTGAGGAG ATAAGGCAA TAAAGGCCA GAGACATGGA 180
 AAAACTGTGA GAGTGTCTGA TGCAGTGAAA GTCAGGAAA AATTTTGGG AAGGGAAGTT 240
 GAAGTCTGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAATA 300
 AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
 CTCATAGACA AGGCCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAACTT CCTTGCCCTT 420
 GATATTGAAA CGTTTATCA TGAGGAGAT GAATTTGAAA AGGCGGAGAT AATAATGATT 480
 AGTTATGCCG ATGAAGAAGA GGGCAGAGTA ATCACATGGA AAAATATCGA TTGCGCGTAT 540
 GTCGATGTTG TGTCCAATGA AAGAGAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
 AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
 AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
 CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
 GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
 TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
 TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGCA 960
 ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
 CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGAGTG GTATCTTTTA 1080
 AGGCTGGCAT ACGCGAGGAA TGAAGTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
 CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAG AGCCAGAAA AGGTTGTGG 1200
 GAAAAATATCA TTATTTTGA TTTCGCGAGT CTGTACCCTT CAATAATAGT TACTCACAA 1260
 GTATCCCCAG ATACCCCTGA AAAAGAGGGC TGTAAGAAAT ACGATGTTGC TCCGATAGTA 1320
 GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCTT CCATCTCGG GGACTTAATT 1380
 GCAATGAGGC AAGATATAAA GAAGAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
 ATGCTCGATT ATAGGCAAG GGTATTTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
 GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTCTG AAAGCGTTAC CGCATGGGG 1560
 AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTGGGCTT TAAGGTTCTT 1620

134/186

TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAA 1680
 AAGAAAGCCA AGGAATTCTT AAACCTACATA AACTCCAAC TTCCAGGTCT GCTTGAGCTT 1740
 GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
 GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGAGTGAG 1860
 ATAGCTAAGG AGACTCAGGC AAAGTTTAA GAGCTATAC TTAAGAGGG AAGTGTGAA 1920
 AAAGCTGTAG AAGTTGTTAG AGATGTTGA GAGAAATAG CAAATATACAG GGTCCACTT 1980
 GAAAGCTTG TTATCCATGA GCAGATTACC AGGATTTAA AGGACTACAA AGCCATTGGC 2040
 CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGA TAAAGTGAA ACCGGCACA 2100
 ATATATAGCT ATATCGTCT CAAAGGGAGC GGAAGATTA GCGATAGGT AATTTACTT 2160
 ACAGAAATACG ATCCTAGAAA ACACAAGTAC GATCCGACT ACTACATAGA AAACCAAGTT 2220
 TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
 CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

Deep Vent - Sac7d DNA polymerase fusion protein (Fig. 17-AAA)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG ACGCTGACTA CATCACCAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
 AAAGAAAACG GCGAGTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTACGCT 120
 CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGAAGA TAACCGCCGA GAGGCATGG 180
 AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCCTGG GAGCCGATT 240
 GAGGTATGGA GCGTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
 AGAGAGCAIT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC 360
 CTAATAGACA AAGCCTTAAT TCCAATGAA GCGGATGAAG AGCTCAAGTT GCTCGCATTT 420
 GACATAGAAA CCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA 480
 AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGA AAAAGATCGA TCTCCCGTAC 540
 GTCGAGGTAG TTTCAGCGA GAGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGAG 600
 AAAGATCCCG ATGTTATAAT TACCTACAAC GCGGATCTT TCGACCTTCC CTATCTAGTT 660
 AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG 720
 ATGCAGAGGC TTGGGGATAT GACACGGGTG GAGATPAAAG GAAGGATACA CTTGACCTC 780
 TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCTCGAGGC AGTTATGAG 840

135/186

Fig. 17 AAA (cont)

GCAATCTTCG GAAAGCCAAA GGAGAAGTT TACGCTCAG AGATAGCTGA GGCCCTGGAG 900
 ACTGGAAGG GACTGGAGAG AGTTGCAAG TATCAATGG AGGATGCAA GTTAACGTAC 960
 GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
 CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
 GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGGAAG 1140
 CTAAGGAGAG GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGAGGGG 1200
 TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCTTCGATPA TAATCACCCTA TAACGTCTCA 1260
 CCGGATACGC TGAACAGGGA AGGGTGTAG GAATACGATG TCGCCCCAGA GGTGGGCAC 1320
 AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA 1380
 AGGCAAGAAA TAAAAAGGAA GATGAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT 1440
 GATTACAGGC AACGGGCAAT CAAATTCCTG GCAACACAGCT ATTATGGGTA TTATGGGTAC 1500
 GCAAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGAGGGAA 1560
 TATATAGAGT TCGTAAGGAA GGAACCTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA 1620
 GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGAGAT AAAGAAGAAA 1680
 GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCAG GGTGTTGA GCTTGAGTAC 1740
 GAGGCTTCT ACGTAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCCGT GATAGATGAG 1800
 GAAGGGAAGA TAATCACTAG GGGGCTTGA ATAGTCAGGA GGGACTGGAG CGAATAAGCC 1860
 AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCTTAAAGC ATGGCAACGT TGAGGAGGCA 1920
 GTAAGAGTAG TTAAGAGAGT AACTGAAAAG CTGAGCAAGT ACGAATATACC TCCAGAAAAG 1980
 CTAGTTATT ACAGCAGAGT CACGAGGCC CTTCACGAGT ACAAGGCTAT AGTCCGCAC 2040
 GTTGCCGTG CAAAAAGGT AGCCGCTAGA GGAGTAAAG TGAGGCCCTG CATGGTATA 2100
 GGGTACATAG TGCTGAGGG AGACGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
 TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220
 GCCGTTCTTA GAATATTAGA GGCCTTTGG TACAGGAAG AAGACCTCAG GTGGCAGAAG 2280
 ACTAAACAGA CAGTCTTAC GGCATGGCTT AACATCAAGA AGAAG // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

Sac7d - Deep Vent DNA polymerase fusion protein (Fig. 17-BBB)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

//ATGATACTTG ACGCTGACTA CATCACCAG GATGGGAGC CGATTATAAG GATTTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAG ATGACTCGCA GATTGATGAG GTTAGGAGA TAACCGCCGA GAGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC 360
CTAATAGACA AAGCCTAAT TCCAATGAA GGCAGTGAAG AGCTCAAGTT GCTCGCATTT 420
GACATAGAAA CCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGA AAAAGATCGA TCTCCCGTAC 540
GTCGAGGTAG TTTCACGCGA GAGGAGATG ATAAAGCGT TCCTCAAGT GATAAGGAG 600
AAAGATCCCC ATGTTATAAT TACCTACAAC GCGGATTCTT TCGACCTTCC CTATCTAGTT 660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG 720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATPAAAG GAAGATACA CTTTGACCTC 780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCTCGAGGC AGTTTATGAG 840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCAG AGATAGCTGA GGCCTGGAG 900
ACTGGAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAA GGTAAAGTAC 960
GAGCTCGGTA GGGAGTTCTT CCCAATGAG GCCCAGCTTT CAAGTTAGT CGGCCAGCCC 1020
CTGTGGGATG TTTCTAGGTC TTCACTGGC AACTTGGTGG AGTGTAACCT CTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAC AAGCCGGATG AGAGGAGTA CGAGAGAAAG 1140
CTAAGGAGA GCTACGCTGG GGGATACGTT AAGAGCCGG AGAAAGGCT CTGGAGGGG 1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCTCGATAA TAATCACCCA TAACGTCTCA 1260
CCGATACGC TGAACAGGA AGGGTGTAG GAATACGATG TCGCCCCAGA GGTGGGCAC 1320
AAGTTCTGCA AGGACTTCCC GGGGTTATC CCCAGCCTGC TCAAGAGGTT ATTGATGAA 1380
AGGCAAGAAA TAAAGAGAA GATGAAGCT TCTAAGACC CAATCGAGAA GAAGATGCTT 1440
GATTACAGGC AACGGCAAT CAAAATCCTG GCAACAGCT ATTATGGGTA TTATGGTAC 1500

137/186

GCAAAAGCCC GTTGTTACTG TAAGAGTGC GCAGAGACG TTACGGCCTG GGGAGGAA 1560
 TATATAGAGT TCGTAAGGAA GGAAGTGGAG GAAAGTTG GGTCAAGT CTTATACATA 1620
 GACACAGATG GACTCTACGC CACAATTCCT GGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680
 GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCAG GCGTGTGGA GCTTGAGTAC 1740
 GAGGCTTCT ACGTAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGT GATAGATGAG 1800
 GAAGGAGA TAATCACTAG GGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAATAAGCC 1860
 AAAGAAACCC AAGCAAAAGT CCTAGAGCT ATCCTAAGC ATGGCAACGT TGAGGAGCA 1920
 GTAAGATAG TTAAGAGGT AACTGAAAG CTGAGCAAGT ACGAATACC TCCAGAAAAG 1980
 CTAGTTATT ACGAGCAGAT CACGAGGCC CTTACGAGT ACAAGCTAT AGTCCGCAC 2040
 GTGCCCCTG CAAAAAGTT AGCCGCTAGA GGAGTAAAG TGAGCCTGG CATGGTATA 2100
 GGGTACATAG TGCTGAGGG AGACGGGCC ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
 TTGATCTCA GGAAGCATAA GTATACGCT GAGTATTACA TAGAAATCA GGTTTACCT 2220
 GCCGTCTTA GAATATTGA GCCCTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAA 2280
 ACTAAACAGA CAGGCTTAG GGCATGCTT AACATCAAGA AGAAG TAA 2328

JDF-3 - Sac7d fusion protein (Fig. 17-CCC)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAAGATGAAAGCCGTCATCAGGTTCTCAAGAAGAGAACCGGAGTTCAAGATTGAATACGACCGGAGTTGAGCCCTACTTCT
 ACGCGCTCTCAGGAGCACTCTGCCATCGAAGAAATCAAAAAGATAACCGGAGAGCAACGGAGGTTAGGTTAAGCGCGGAGAAAGTTGAAGAAAAGTTCCCTCG
 CAGGTTGTGAGGTTCTGGTCTCTACTTACCGCACCCGAGAGACXXXCCGCCAATCCCGACAAAATAAGAAAGCAACCCCGGTTATCGACATCTACGAGTACGACATACC
 TTCGCCAAGCGCTACCTCATAGACAAAGGCCCTAATCCCGATGGAAGTTGAGGAGAGCTTAACTCATGTCTTCCGATCCGAGACGCTCTACCAAGAGGAGATTGGA
 CCGGGCCGATTCTGATGATAAGCTACGCCGATGAAGCGAGCGCGGTGATTAACCTGGAAGAAGATCGACCTTCTTACGTTGAGTTGTCTCCACCGAAGAGATGATTAA
 GCGCTTCTGAGGTTCTTAAGAGAGAACCCGACCTGCTGATAACATCAACGGCGACAATTGCACTTCCCTACCTGAATAAGCGCTGTGAGAACTTGGCGTGAAGCTT
 ACCCTCGGAGGAGCGGAGCGAGCCGAAGATACAGCGCATGGGGACAGGTTTGGCGTCAAGGTTACCGCCGAGAGATAGCCACCGCTGGAGACCGGCGAGGGCTTGAGAG
 ACCTCCGACCTACACCTTGAGGCTGTATACGAGCGGTTTTCGCAAGCCCAAGAGAAGTCTACCGCGAGAGATAGCCACCGCTGGAGACCGGCGAGGGCTTGAGAG
 GGTGCGCGCTACTCGATGAGAGCGGAGGGTTACCTACGAGCTTGGCAGGAGTTCTCCGATGAGGGCCAGCTTTCAGGCTCATCGCCAAAGGCTCTGGAGCGTTCC
 CGCTCCAGCACCGGCAACCTCGTGAAGTGTCTCTTAAGGAAGCCTACGAGAGGAACGAACTCGCTCCCAACAAGCCCGACGAGAGGAGCTGGCGAGAGAGAGGGGGCT
 ACgCCGGTGGCTACGTCAGGAGCGCGGAGCGGAGCTGTGGACAATATCGTATCTAGACTTTCGTAAGTCTTACCTTCAATCATATAACCCCAACAGCTCTCGCAGATAC
 GCTCAACCGGAGGGGTAGAGCTACGACGTTGCCCCGAGGTCGTCACAGTCTTTCGCAAGGACTTCCCGGCTTCATTCGAGCCTGCTCGAAACCTGCTGAGGAAAGG
 CAGAAGATAAAGAGGAAGATGAAGCAACTCTGACCCGCTGGAAGAAGATCTCTCGATTACAGGCCAACGCGCCATCAAGATTCTCGCCAACACAGCTACTACGGCT
 ATGCCAGGGCAAGATGTTACTGACGAGGAGTGCAGAGCGTTACGCGCATGGGAAGGAGTACATCGAATGTTTCATCAGAGAGCTTGAGGAAAGTTCCGTTTAAAGTCT
 CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACCTGAACAAGTCAAGAAAAGGCAATGGAATTCTTAACTATATCAATCCCAACTGCCGCTTCTC
 GAACTCGAATACGAGGCTTCTACGTACGAGGCTTCTTCGTACGAAAGAAAAGTACCGCGTCAATCGAGAGGAGGCAAGATAACACAGCGCGGCTTGAGATAGTACGGCGG
 ACTGGAGCGAGATAGCGAAGGAGACCGCAGGCGGTTTGGAGGCGATCTACGGCACGGTGAAGAGCGCTCAGAAATTGTACGGGAAGTCAACGAAAAGCTGAGCAA
 GTACGAGGTTCCGCGGAGAAAGCTGTTATCCACGACAGATACGCGCGAGCTCAAGGACTACAGGCCACCGGCGGACGTAAGCATAGCGAAGcGTTTGGCCGCCAGAGGT

138/86

Fig. 17 DDD (cont)

GTGTTAAATCCGGCCGGAAGTGTAGCTACATCGTTCTGAAGGCTCCGGAAGATAGGCGACAGGCGATTCCCTTCGACGAGTTGACCCGACGAAGCACAGTACGA
TCCGACTACTACATCGAGAACAGGTTCTGCCGCGAGTTGAGAGATCCTCAGGGCTTCGGCTACCGCAAGGAAGACCTGCGCTACGAGAGACGAGGCAAGTCCGGCTTGGC
GCGTGGCTGAAGCCGAAGGGGAAGAAGAGTGA

140/86

Synthetic Sso7d gene: (Fig. 17-EEE)

A T V K F K Y K G E E K E V D I S K
GCA ACC GTA AAG TTC AAG TAC AAA GCC GAA GAA AAA GAG GTA GAC ATC TCC AAG
I K K V W R V G K M I S F T Y D E G
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
G G K T G R G A V S E K D A P K E L
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
L Q M L E K Q K K
CTG CAG ATG CTG GAG AAG CAG AAA AAG

Sso7d-Taq DNA polymerase fusion protein (Fig. 17-FFF)

// A T V K F K Y K G E E K E V D I S K
// GCA ACC GTA AAG TTC AAG TAC AAA GCC GAA GAA AAA GAG GTA GAC ATC TCC AAG
I K K V W R V G K M I S F T Y D E G
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
G G K T G R G A V S E K D A P K E L
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
L Q M L E K Q K K // G G G
CTG CAG ATG CTG GAG AAG CAG AAA AAG // GGC GGC GGT

V T S G M L P L F E P K G R V L L V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG
D G H H L A Y R T F H A L K G L T T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC
S R G E P V Q A X Y G F A K S L L K
AGC CCG GGG GAG CCG GTG CAG GCG OTC TAC GGC TTC GCC AAG AGC CTC CTC AAG
A L K E D G D A V I V V F D A K A P

14/1/86

Fig. 17 FFF (cont)

GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC
 S F R H E A Y G G Y K A G R A P T P
 TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCC GGC CGG GCC CCC ACC CCA
 E D F P R Q L A L I K E L V D L L G
 GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG
 L A R L E V P G Y E A D D V L A S L
 CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG
 A K K A E K E G Y E V R I L T A D K
 GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA
 D L Y Q L L S D R I H V L H P E G Y
 GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC
 L I T P A W L W E K Y G L R P D Q W
 CTC ATC ACC CGC GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG
 A D Y R A L T G D E S D N L P G V K
 GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG
 G I G E K T A R K L L E E W G S L E
 GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA
 A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG
 A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
 L P L E V D F A K R R E P D R E R L
 CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
 L E S P K A L E E A P W P P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CGG CGG GAA GGG GCC

14/2/86

Fig. 17 FFF (cont)

F V G F V L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
L A A A R G G R V H R A P E P Y K A
CTG GCC GCC AGG GGG GGC CGG GTC CAC CGG GCC CCT TAT AAA GCC
L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CGG GGT CTT CTC GCC AAA GAC CTG AGC GTT CTG
A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
Y L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG TAC GGC
G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC
A N L W G R L E G E E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG
E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG
R L D V A Y L R A A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
A R L E A E V F R L A A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC
S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC
G K T E K T G K R S T S A A V L E A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTG GAG GCC
L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC
K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

143/186

Fig. 17 FFF (cont)

G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC ACG GGC AGG CTA AGT
 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG
 I R R A F I A E E G W L L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT
 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC
 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC
 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC
 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC
 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC
 K V R A W I E K T L E E G R R R G Y
 AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC
 V E T L F G R R R Y V P D L E A R V
 GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
 K S V R E A A E R M A F N M P V Q G
 AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
 T A A D L M K L A M V K L F P R L E
 ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
 E M G A R M L L Q V H D E L V L E A
 GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
 P K E R A E A V A R L A K E V M E G

14/4/86

CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

L S A K E G I D G R G G G G H H H H
CTC TCC GCC AAG GAG GCG ATT GAT GGC CGC GGC GGA GGC GGG CAT CAT CAT CAT

H H *
CAT CAT TAA

Pfu DNA Polymerase (W1) -Sso7d fusion protein (Fig. 17-GGG)

//

ccctgtcct gggtccacat atatgttctt actgccttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tcccaccaccg cccaagaagg ttatttctat
caactctaca cctccccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttactt ccaaaactgag ttagtagata tgtggggagc ataagtattt tagatgtgga
ttacataact gaagaaggaa aacctgttat tagctatlc aaaaagagaa acggaaaatt
taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgatlc
aaagattgaa gaagttaaga aaataacggg ggaagggcat ggaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaacttta
tttggaacat cccaagatg ttcccactat tagagaaaa gttagaagac atccagcagt
tgtgacatc ttcgaatagc atattccatt tgcaagagaa taccctacgc acaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa

145/86

Fig. 17 GGG (cont)

tgaagcaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgaagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatgagagact cattcgactt cccatattta gcgaaaaggg cagaaaaaact
tgugattaaa ttaaccattg gaagagatgg aaagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggagaagat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttgaaaagcc
aaagagagaag gtatacgccg acgagatagc aaaaagccctgg gaaagtggag agaaccctga
gagagttgcc aaatactcga⁴⁴ tggaaagatgc aaagccaact tatgaactcg ggaagaatc
cctccaatg gaaattcagc ttcaagatt agttggaca ccttatggg atgtttcaag
gtcaagcaca gggaaacctg tagagtgtt ctacttagg aaagcctacg aaagaaaacga
agtagctcca aacaagccca gtgaagaggga gtatcaaaaga aggcctcaggg agagctacac
aggtggaatc gttaaagagc cagaaaaaggg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttatattac ccacaatgtt tctcccgata ctctaattc
tgaaggatgc aagaactatg atatcgctcc tcaagtaggc cacaaattct gcaaggacat
ccctggtttt ataccagtc tcttgggaca ttgttagag gaaagacaaa agatlaagac
aaaaaatgaa gaaactcaag atcctataga aaaaatactc ctgactata gacaaaaagc
gataaaaactc ttagcaaatc cttctacgg atattatggc tatgcaaaag caagatgta
ctgtaaggag tgtgtctgaga gcgttactgc ctggggaga aagtacatcg agttaagt
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atgtctcta
tgcaactatc ccaggagag aaagtgagg aataagaaa aaggtcttag aattgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag

146/86

Fig. 17 GGG (cont)

gggatctctc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggaagagattg gaagtgaatt gcaaaagaaa ctcaagctag
agttttgga gacaatactaa aacacggaga tgttgagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaat tccaccagag aagctcgcaa tatatgagca
gataaccaaga ccatcacatg agtataaggc gatagtcct cagctagctg ttgcaaaaga
actagctgct aaaggagtta aaataaagcc aggaatggtta attggataca tagtacttag
aggcgagtgt ccaattagca ataaggcaat tctaactgag gaatacgatc ccaaaaagca
caagtatgac gcagaatat acattgagaa ccagttctt ccagcggtag ttaggatatt
ggagggattt ggatacagaa aggaagacct cagatacca aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatcccta gaaaaggcat agatatcaac tttattctt
tcctaaccctt ttctatgaaa gaagaaactga gcaggaatta ccagttctc cgltattta
tggttaatta aaaaccatg ctctgggag aatcttcgaa taaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcaattcaa accccttcgt tagaatggt
ctatctgcat gcttctctgg ctcggaanng gaggttcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaacttga cttctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa ttgcgagac gtagatcttt
tttgctccaa gcagagccgc tccaatgcat aacacccctg ttcccgcaac caagtccgct
acaattttt cctgtatct cctaattgat aagcaagcca aaggagagta gatgtaacct
ttccgggagt ttgttatgc tctagccaag gtttgggatt ttgaaacct ttaactctgg
aaagtataat ttcaagctcc ttcttctca tgacagatga aaatgtttt tgtctcttt

14/1/80

taacttttac agaataact gtctcaatt atgacaactc ttgacattt tacttcatta
ccagggtaat gttttaagt atgaatttt tcttccatag aggaagnnn nngtcctc
ctcgatttcc ttggtgtgc tccatgatg aagcttccaa agtgggtgt cagacttta
gacctcaaa taccagacga caatggtgtg ctcaactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgtgttagc tcntccnga
aagattgaga tgttcttg //

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

PFU DNA POLYMERASE (V93 R OR E)-Sso7d fusion protein (Fig. 17-HHH)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGATTA CATACTGAA GAAGGAAAC CTGTATTAG GCTATCAAA 60 AAAGAGAAG GAAATTAA GATAGACAT
GATAGAACTT TTAGACCATTA CATTACGCT 120 CTCTCAGGG ATGATTCAA GATTGAAGAA GTTAGAATAA TAAAGGGGA AAGCATGGA 180
AAGATTGTA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTCTCGG CAAGCCTATT 240 ACCGTGGA AACTTTATT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
CTCATCGACA AAGCCTAAT ACCAATGAG GGGAGAAG AGCTAAGAT TCTGCCCTC 420 GATATAGAAA CCCTCTATCA CGAAGAGAA
GAGTTTGAA AAGCCCAAT TATAATGATT 480 AGTTATGAG ATGAATAATG AGCAAGGTG ATTACTTGA AAAACATAGA TCTTCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGAG 600 AAGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTCCC ATATTAGCG 660 AAAAGGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGA GAGATGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGCGATAT GACGCTGTA GAAGTCAAGG GAAGATACA TTGCACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTG GAAAGCCAAA GGAGAGGTA TACGCCGACG AGATAGCAAA AGCCTGGAA 900
AGTGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCACCTTAT 960 GAACTCGGA AAGAATTCCT TCCAATGAA
ATTGAGCTTT CAAGATTAGT TGGACAACCT 1020 TTAAGGATG TTTCAAGGTC AAGCACAGGG AACCTGTAG AGTGGTCTT ACTTAGGAAA
1080 GCCTAGAAA GAAACGAAGT AGCTCCAAC AAGCCAAGTG AAGAGAGTA TCAAGAAGG 1140 CTCAGGAGA GCTACACAGG
TGATTCGTT AAAGAGCCAG AAAAGGGTT GTGGAAAAC 1200 ATAGTATACC TAGATTTAG AGCCTATAT CCCTGATTA TAATTACCA
CAATGTTCT 1260 CCCGATCTC TAAATCTGA GGGATGCAAG AACTATGATA TCGCTCTCA AGTAGCCAC 1320 AAGTTCTGA

148/86

GAAAAGTTTG GATTAAAGT CCTTACATT 1620 GACACTGATG GTCTTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG
 1680 GCTCTAGAAT TTGTAATAA CATAAATCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGTTTT ATAAGAGGG
 ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAAG TCATTACTCG TGGTTAGAG ATAGTTAGGA GAGATTGGAG
 TGAATTTGCA 1860 AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGAGATGT TGAAGAAGCT 1920 GTGAGAATAG
 TAAAAGAAGT AATACAAAAG CTGGCAATT ATGAATTCC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT
 ATAAGGCAT AGTCCCTCAC 2040 GTAGCTGTG CAAAGAACT AGCTGCTAAA GAGTTAAAA TAAAGCCAGG AATGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA GTATGACCA
 GAATATTACA TGGAGAACCA GGTTCCTCCA 2220 GCGTACTTA GATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG
 2280 ACAAGACAAG TCGGCTTAC TTCCTGGCTT AACATTAAAA AATCC // 2328

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
 ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
 GGT GGC AAG ACC GGC CGT GGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
 CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

PFU DNA POLYMERASE(D141A/E143A/V93R OR E)-Sso7d fusion protein (Fig. 17-

III)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGATTA CATACTGAA GAAGGAAAC CTGTATTAG GCTATTCAA 60 AAAGAGACG GAAATTTAA GATAGACAT
 GATAGAACTT TTAGACCATA CATTACGCT 120 CTCTCAGG AGATTCAA GATTGAAGAA TAAAGGGGA AAGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTCTCGG CAAGCCTATT 240 ACCGTGTGA AACTTTATT GGAACATCCC
 CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
 CTCAATGACA AAGGCCTAAT ACCAATGAG GGGGAAGAAG AGCTAAAGAT TCTGCCCTTC 420 GCNATAGCNA CCTCTATCA CGAAGGAGAA
 GAGTTTGAA AAGGCCAAT TATAATGATT 480 AGTTATGAG ATGAAATGA AGCAAGGTG ATTACTTGA AAAACATAGA TCTTCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAGAGAT TTCTCAGGAT TATCAGGAG 600 AAGATCCTG ACATTATAGT TACTTATAAT
 GGAGACTCAT TCGCATTCCC ATATTAGCG 660 AAAAGGCGAG AAAAACTTGG GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGCGATAT GACGCTGTA GAAGTCAAGG GAAGATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
 CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGA 900
 AGTGAGAGA ACCTTGAGAG AGTTGCCAAA TACTGATGG AAGATGCAA GGCACCTTAT 960 GAACTCGGA AAGAATTCTT TCCAATGGA
 ATTCAAGCTT CAAGATTAGT TGGACAACCT 1020 TTATGGATG TTTCAGGTC AAGCACAGG AACCTTGTAG AGTGTTCTT ACTTAGGAAA
 1080 GCCTACGAAA GAAACGAAGT AGCTCCAAC AAGCCAAGT AAGAGAGTA TCAAGAAAG 1140 CTCAGGAGA
 GCTACACAGG.TGGATTCGTT AAAGAGCCAG AAAAGGGTT GTGGAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATT
 TAATTACCA CAATGTTTCT 1260 CCCGATCTC TAAATCTGA GGGATGCAAG AACTATGATA TCGCTCTCA AGTAGGCCAC 1320
 AAGTTCTGA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGA 1380 AGACAAAGA TTAAGACAA AATGAAGGA
 ACTCAAGATC CTATAGAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAATTCTT TCTACGATA TTATGCTAT
 1500 GCAAAAGCAA GATGTACTG TAAGAGTGT GCTGAGAGC TTACTGCCTG GGAAGAAAG 1560 TACATCGAGT TAGTATGGA

150/186

CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGACATA 1200
 GTGTACCTAG ATTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTGCCG 1260
 GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
 TTCTGCAAGG ACTTCCAGG ATTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
 CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCGA TCGAGAGGAA GCTCCTCGAT 1440
 TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTACTA CGGCTATGCA 1500
 AGGCGCGCT GTTACTGCAA GAGTGTGCA GAGAGCGTAA CGGCTGGGG AAGGAGTAC 1560
 ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
 ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
 ATGAGTTCC TCAAGTATAT CAACGCCAAA CTTCGGGGCG CGCTTGAGCT CGAGTACGAG 1740
 GCGTTCTACA AACCGGCTT CTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
 GGCAGATTA CAACGCGCG ACTTGAGATT GTGAGCGGTG ACTGAGCGA GATAGCGAAA 1860
 GAGACGCAGG CGAGGTTCT TGAAGCTTGG CTAAGGACG GTGACGTCGA GAAGGCCGTG 1920
 AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
 GTGATCCACG AGCAGATAAC GAGGATTTA AAGACTACA AGGCAACCGG TCCCCACGTT 2040
 GCCGTTGCCA AGAGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
 TACATCGTGC TCAAGGCTC TGGGAGATA GCGACAGGG CGATACCGTT CGACGAGTTC 2160
 GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAAGT TCTCCAGCC 2220
 GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCCGTA CCAGAAGACG 2280
 AGACAGGTTG GTTTGAGTGC TTGCTGAAG CCGAAGGAA CT 2325

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
 ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
 GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
 CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

Sso7d - KOD DNA POLYMERASE fusion protein (Fig. 17-11.1)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
 ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
 GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
 CTG CAG ATG CTG GAG AAG CAG AAA AAG //

//ATGATCCTCG ACACTGACTA CATAACCGAG GATGAAAGC CTGTACATAAG AATTTCAAG 60
 AAGGAAAACG GCGAGTTAA GATTGAGTAC GACCGGACTT TTGAACCTA CTCTACGCC 120
 CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACGGCCGA GAGGCACGGG 180
 ACGGTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCTCCGG GAGACCAAGT 240

GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
 CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
 CTCTATAGACA AGGATTAGT GCCAATGGAA GCGCAGCAGG AGCTGAATAAT GCTCGCCTTC 420
 GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
 AGCTACGCCG ACGAGGAAGG GGGCAGGGTG ATAATTGA AGAACGTGA TCTCCCTAC 540
 GTTGACGTCG TCTCGACGGA GAGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
 AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGCACAAC TCGACTTCGC CTATCTGAAA 660
 AAGCGCTGTG AAAAGCTCGG AATAAATTG GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
 ATTCAGAGGA TGGCGACAG GTTTCGGTC GAAGTGAAG GACGATACA CTTCGATCTC 780
 TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
 GCCGTCTTCG GTCAGCCGAA GGAGAAGTT TACGCTGAGG AAATAACCA AGCCTGGAA 900
 ACCGGCGAGA ACCTTGAGAG AGTCGGCCGC TACTCGATGG AAGATGCGAA GGTACATAC 960
 GAGCTTGGGA AGGAGTTCTT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
 CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCTT CCTCAGGAAG 1080
 GCCTATGAGA GGAATGAGCT GGGCCCGAAC AAGCCCGAATG AAAAGGAGCT GGCCAGAAGA 1140
 CGGCAGAGCT ATGAAGGAGG CTATGTAATA GAGCCCGAGA GAGGTTGTG GGAGAACATA 1200
 GTGTACCTAG ATTTAGATC CCTGTACCCC TCAATCATCA TCACCACAA CGTCTCGCCG 1260
 GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGAGT CGGCCACCGC 1320
 TTCTGCAAGG ACTTCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
 CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
 TACAGGCAGA GGGCCATCA GATCCTGGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
 AGGGCGCGCT GTACTGCAA GAGTGTGCA GAGAGCGTAA CGGCTGGGG AAGGAGTAC 1560
 ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGTAAAT CTACAGCGAC 1620
 ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
 ATGAGATTCC TCAAGTATAT CAACGCCAAA CTTCGGGCG CGCTTGAGCT CGAGTACGAG 1740
 GGCTTCTACA AACCGGCTT CTTCGTCAGG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
 GGCAGATATA CAACGCGCGG ACTTGAGATT GTGAGCGGTG ACTGAGCGA GATAGCGAAA 1860
 GAGACGCAAG CGAGGGTTCT TGAAGCTTTG CTAAGGAGC GTGACGTGGA GAAGCCGCTG 1920
 AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCGCC GGAGAAAGCTG 1980
 GTGATCCACG AGCAGATAAC GAGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
 GCCGTTGCCA AGAGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
 TACATCGTGC TCAAGGCTC TGGGAGGATA GCGCAGAGG CGATACCGTT CGACGAGTTC 2160
 GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATG AGAACCAAGT TCTCCAGGCC 2220
 GTTGAGAGAA TTCTGAGAGC CTTCGCTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
 AGACAGGTTG GTTGAGTGC TTGGCTGAAG CCGAAGGGA CT //TAG 2325

Sso7d-Vent DNA POLYMERASE FUSION PROTEIN (Fig. 17-MMM)

Fig. 17 MMM (cont)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG //

ATGATACTGG ACACTGATTA CATACAAAA GATGGCAAGC CTATATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGCCAA TAAAGGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGTCTGA TGCAGTGAAA GTCAGGAATA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCAITCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGCGTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAAGT CCTTGCTTTT 420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTTGGA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGGCAGAGTA ATCACATGGA AAAATATCGA TTGCGCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
AAAGACCCCG ATGTGATTAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTGCGCTT GTCTTAGGAA GGGACAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTT GTGTGGAAT TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAAACAG AAGAAAGCAT GAATAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACCTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAG AGCCAGAAAA AGTTTGTGG 1200
GAAAATATCA TTTATTGGA TTTCGCGAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCCTGA AAAAGAGGGC TGTAAGAAAT ACGATGTGCT TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCTT CCATACTCGG GGAATTAAAT 1380
GCAATGAGGC AAGATATAAA GAAGAAAAATG AAATCCACAA TTGACCCGAT CGAAAAAGAAA 1440
ATGCTCGATT ATAGGCAAGG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGTTCTT 1620
TATGCGGACA CTGACGGCTT TTAATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAG 1680
AAGAAAGCCA AGGAATTCCT AAACCTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATTAAC AACCAAGGGC TTGCAAGTAG TAAAGAGAGA TTGAGGTGAG 1860

154/86

ATAGCTAAGG AGACTCAGGC AAAGTTTGA GAGCTATAC TTAAGAGGG AAGTGTGAA 1920
 AAAGCTGTAG AAGTTGTTAG AGATGTGTA GAGAAATAG CAAATATACAG GGTTCACCTT 1980
 GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTAA AGGACTACAA AGCCATTGGC 2040
 CCTCATGTGG CGATAGCAAA AAGACTTGCC GCAAGAGGA TAAAGTGAA ACCGGCACA 2100
 ATAAATAGCT ATATCGTCT CAAAGGAGC GGAAGATAA GCGATAGGT AATTACTT 2160
 ACAGAATACG ATCCTAGAAA ACACAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
 TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
 CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAGA GGTAG 2325

Vent DNA POLYMERASE - Ss07d FUSION PROTEIN (Fig. 17-NNN)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACACGTGATTA CATAACAATA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
 AAAGAGAAGC GGGAGTTTAA AATAGAAGCTT GACCTTCATT TTCAGCCCTA TATATATGCT 120
 CTCTCAAGAG ATGACTCCGC TATTGAGGAG ATAAGGCCAA TAAAGGCCA GAGACATGGA 180
 AAAACTGTGA GAGTGTCTGA TGCAGTGAAA GTCAGGAAA AATTTTGGG AAGGGAAGTT 240
 GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
 AGGGAACATC CAGCTGTGTG TGACATTTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
 CTCATAGACA AGGCGTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAAGT CCTTGCCTTT 420
 GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTTGAAA AGGCGAGAT AATAATGATT 480
 AGTTATGCCG ATGAAGAAGA GGGCAGAGTA ATCAGATGGA AAAATATCGA TTGCCGTAT 540
 GTCCATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
 AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
 AAACGGGCAG AAAAGCTGGG AGTTCCGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
 CCCAAGATTG AGAGGATGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
 GATCTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
 TATGAAGCAG TTTTAGGAAA AACCAAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
 TGGGAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
 ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
 CAAAGTGTAT GGGACGCTC GAGATCAAGC ACCGGCAACC TCGTGAGTG GTATCTTTTA 1080
 AGGTTGGCAT ACGCGAGGAA TGAAGTTGCA CCGAACAAC CTGATGAGGA AGAGTATAAA 1140
 CGGCGCTTAA GAACAACCTTA CCTGGGAGGA TATGTAAAG AGCCAGAAA AGGTTGTGG 1200
 GAAATATCA TTATTTGGA TTTCGCGAGT CTGTACCTT CAATAATAGT TACTCACAAC 1260
 GTATCCCCAG ATACCTTTGA AAAAGAGGGC TGTAGAATT ACGATGTTGC TCCGATAGTA 1320
 GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCT CCATACTCGG GGACTTAATT 1380
 GCAATGAGGC AAGATATATA GAAGAAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
 ATGCTCGATT ATAGGCAAG GGTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
 GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560

155/86

AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTGGCTT TAAGTTCTT 1620
 TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCAITAA 1680
 AAGAAAGCCA AGGAATTCCCT AAACCTACATA AACTCCAAC TTCCAGTCT GCTTGAGCTT 1740
 GAGTATGAGG GCTTTACTT GAGAGGATTC TTGTGTACAA AAAAGCGCTA TGCAGTCATA 1800
 GATGAAGAGG GCAGGATTAAC AACCAAGGGC TTGGAAGTAG TAAAGAGAGA TTGGAGTGAG 1860
 ATAGCTAAGG AGACTCAGGC AAAGGTTTAA GAGGCTATAC TTAAAGAGGG AAGTGTGAA 1920
 AAAGCTGTAG AAGTTGTAG AGATGTTGTA GAGAAAATAG CAAATACAG GGTTCACCTT 1980
 GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTTAA AGGACTACAA AGCCATTGGC 2040
 CCTCATGTCC CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAGTGAA ACCGGCACA 2100
 ATATTAAGCT ATATCGTCT CAAAGGAGC GGAAGATTA GCGATAGGGT AATTTTACTT 2160
 ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
 TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTGGATACA GAAAGAGAGA TTTAAGGTAT 2280
 CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
 ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
 GGT GGC AAG ACC GGC CGT GGT GGT GGT GGT GGT GGT GGT GGT GGT GGT GGT GGT
 CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

Deep Vent- Ssod7 DNA polymerase fusion protein (Fig. 17-000)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG ACGCTGACTA CATCACCAGG GATGGGAAGC CGATTATAAG GATTTCAAG 60
 AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTACGCT 120
 CTCCCTCAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGG 180
 AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT 240
 GAGGTATGGA GCGTGTACTT TGAACACCCCT CAGGACXXXC CCGCAATAG GATAAGATA 300
 AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCGTTCCG GAAGAGGTAC 360
 CTAATAGACA AAGGCCTAAT TCCAATGGA GGCATGAAG AGCTCAAGTT GCTCGCAATT 420
 GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGCCCAT TATAATGATA 480
 AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGA AAAAGATCGA TCTCCCGTAC 540
 GTCGAGGTAG TTTCACGCGA GAGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGAG 600
 AAAGATCCCG ATGTTATAAT TACCTACAAC GCGATTTCT TCGACCTTCC CTATAGTT 660
 AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG 720
 ATGCAGAGGC TTGGGGAATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
 TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTGAGGC AGTTTATGAG 840
 GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCAG AGATAGCTGA GGCTGGGAG 900
 ACTGGAAGG GACTGAGAG AGTTGCAAG TATTCAATG AGGATGCAAA GGTAAACGTAC 960
 GAGCTCGGTA GGGAGTTCTT CCCAATGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
 CTGTGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTG AGTGTACCT CCTCAGGAAG 1080

156/86

GCCTACGAGA GGAATGAATT GGCTCCAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG 1140
 CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGAGCCGG AGAAGGGCT CTGGAGGGG 1200
 TTAGTTCCC TAGATTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA 1260
 CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTGGGCAC 1320
 AAGTTCTGCA AGGACTTCCC GGGGTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA 1380
 AGGCAAGAAA TAAAAAGGAA GATGAAGCT TCTAAGACC CAATCGAGAA GAAGATGCTT 1440
 GATTACAGGC AACGGCAAT CAAATCCTG GCAACAGCT ATTATGGTA TTATGGGTAC 1500
 GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGAGGGAA 1560
 TATATAGAGT TCGTAAGGAA GGAAGTGGAG GAAAGTTTCG GGTTCAAAGT CTTATACATA 1620
 GACACAGATG GACTCTACGC CACAATTCTT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680
 GCCCTAGAGT TCGTAGATTA TATAACGCC AAGCTCCAG GGCTGTTGA GCTTGAGTAC 1740
 GAGGGCTTCT ACGTAGAGG GTTCTTCGTG ACGAAGAGA AGTATGCGTT GATAGATGAG 1800
 GAAGGGAAGA TAATCAGTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAATAGACC 1860
 AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAGC ATGGCAACGT TGAGGAGGCA 1920
 GTAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAATATACC TCCAGAAAAG 1980
 CTAGTTATTT ACGAGCAGAT CACGAGGCC CTTCACGAGT ACAAGGCTAT AGGTCCGCAC 2040
 GTTCCCGTGG CAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCTTGG CATGTGATA 2100
 GGGTACATAG TGCTAGAGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
 TTCGATCTCA GGAAGCATTA GTATGACGCT GAGTATTACA TAGAAATCA GTTTTACCT 2220
 GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAG AAGACCTCAG GTGCAGAAAG 2280
 ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG 2328

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
 ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
 GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
 CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

ssod7 - Deep Vent DNA polymerase fusion protein (Fig. 17-PPP)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
 ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
 GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
 CTG CAG ATG CTG GAG AAG CAG AAA AAG //

ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTCAAG 60
 AAAGAAAACG GCGAGTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTACGCT 120
 CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGAAGA TAACGCCCGA GAGGCATGGG 180

157/80

AAGATAGTGA GAATTATAGA TGCCGAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT	240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGAC XX CC CCGCAATAAG GGATAAGATA	300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCTTCGC GAAGAGGTAC	360
CTAATAGACA AAGCCTAAT TCCAATGAA GCGCATGAAG AGCTCAAGTT GCTCGCATT	420
GACATAGAAA CCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA	480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC	540
GTCGAGGTAG TTCCAGCGA GAGGAGATG ATAAGCGGT TCCTCAAGT GATAAGGAG	600
AAAGATCCCG ATGTTATAAT TACCTACAAC GCGGATTCTT TCGACCTTCC CTATCTAGTT	660
AAGAGGCGCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG	720
ATGCAGAGGC TTGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC	780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCTCGAGGC AGTTTATGAG	840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCCTGGAG	900
ACTGGAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAAA GGTAACGTAC	960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC	1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGTACCT CCTCAGGAAG	1080
GCCTACGAGA GGAATGAATT GGTCCCAAC AAGCCGGATG AGAGGAGTA CGAGAGAAGG	1140
CTAAGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGCT CTGGGAGGG	1200
TTAGTTCCC TAGATTTCAG GAGCCTGTAC CCTCGATAA TAATCACCA TAACTCTCA	1260
CCGGATACGC TGAACAGGGA AGGGGTAGG GAATACGATG TCGCCCCAGA GGTGGGCAC	1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA	1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAAGTGCTT	1440
GATTACAGGC AACGGGCAAT CAAATCCTG GCAACACAGCT ATTATGGTA TTATGGGTAC	1500
GCAAAAGCCC GTTGTA CT G TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGAGGGAA	1560
TATATAGAGT TCGTAAGGAA GGAACGTGAG GAAAGTTCC GGTTCAAAGT CTTATACATA	1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA	1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCAG GGCCTGTGA GCTTGAGTAC	1740
GAGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCC TT GATGATGAG	1800
GAAGGGAAGA TAATCACTAG GGGGCTTGA A ATAGTCAGGA GGACTGAG CGAATAGCC	1860
AAAGAAAACC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA	1920
GTAAGATAG TTAAGAGAGT AACTGAAAG CTGAGCAAGT ACGAATACC TCCAGAAAAG	1980
CTAGTTATT ACGAGCAGAT CACGAGGCC CTTACGAGT ACAAGGCTAT AGGTCCGCAC	2040
GTTGCCGTGG CAAAAAGTT AGCCGCTAGA GGAGTAAAG TGAGGCCCTG CATGGTGATA	2100
GGGTACATAG TGCTGAGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG	2160
TTCGATCTCA GGAAGCAATA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT	2220
GCCGTCTTA GAATATTAGA GGCCTTTGGG TACAAGGAAG AAGACCTCAG GTGGCAGAAG	2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA	2328

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAATGGAAGCCCGTCATCAGGGTCTTCAAGAGGAGAACGGCGAGTTCAAGATTGAATACGACCGCGAGTTCGAGCCCTACTCT
ACGGCTCTCAGGGAGCAGCTCTGCCATCGAAGAAATCAAAAGATAACCGGAGAGGACGCGAGGGTCTTAAGTTAAGCGCGGAGAGAGTGAAGAAAGTTCCCTCGG
CAGGTCTGTGAGGTCCTGGTCTCTACTTACGCAACCGCAGGACXXXCCGGCAATCCGGACAAATAAGGAAGCACCCCGGCTCATCGACATCTACGAGTACGACATACCC
TTCCCAAGCGCTACCTCATAGACAAAGGCCATAATCCCGATGGAAGGTGAGGAAGAGCTTAACATCATGTCTTGGACATCGAGACGCTCTACCAAGGAGGAGAGATTGGAA
CCGGCCGATTTGATGATAAGCTACCGCGATGAAGCGAGCGCGGTGATAACCTGGAAGAAGATCGACCTTCCCTTACGTTGAGGTTGTCTCCACCGAAGAGAGATGATTAA
GGCTTCTTGAGGTCGTTAAGGAGAACCGGACGTGCTGATAACATACACGGCGACACTTCCGCTTACCTGAATAAGCGCTGTGAGAAAGCTTGGCGTGAGCTTT
ACCTCGGAGGAGCGGAGCGAGCCGAAGATACAGCGCATGGGGACAGGTTTGGCGTGAAGGTGAAGGGCAGGTTACACTTCGACCTTTATCCAGTCAATAAGCGCACCATAA
ACCTCCGACCTACACCCCTTGAGGCTGTATACGAGCGGTTTTCGGCAAGCCCAAGGAGAGTCTACCGCAGAGATAGCCACCGCTGGAGAACCGGCGAGGCTTGAGAG
GGTCGGCGCTACTCGATGAGGACCGGAGGTTACCTACGAGCTTGGCAGGAGTTCTCCGATGGAAGGCCACGCTTCCAGGCTCATCGGCCAAGGCTCTGGACGTTTCC
CGCTCCAGCACCGGCAACCTCGTGAAGTGTCTCTTAAGGAAGGCTTACGAGAGAACGAACTCGCTCCCAACAGCCGAGAGAGGAGCTGGCGAGAGAGAGGCGGCT
ACGCCGGTGCTACGTCAGGAGCGCGGAGCTGTGGACAATATCGTATCTAGACTTTCGTAGTCTCTACCTTCAATCATATAACCCACAACGTTCTGCCAGATAC
GCTCAACCGCGAGGGGTGAGAGCTACGACGTTGCCCCGAGGTCGGTCAAGGACTTCCCGGCTTCATTCGAGCTCGGAAACCTGCTGGAGGAAAGG
CAGAAGATAAGAGGAAGATGAAGGCAACTCTGACCCGCTGGAAGAATCTCCTCGATTACAGGCAACGCGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT
ATGCCAGGGCAAGATGTTACTGACGGAGTGCCTCGAGAGCGTTACGGCATGGGAAGGAGTACATCGAAATGTCATCAGAGAGCTTGAAGAAAGTTCCGTTTAAAGTCCCT
CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACCTGAACACAGTCAAGAAAGGCAATGAGTTCTTAACTATATCAATCCCAACTGCCCGGCTTCTC
GAATCGAATACGAGGCTTCTACGTCAGGGCTTCTGTCACGAAGAAAGATACCGGTCATCGACGAGGAGGCGCAAGATTAACCAACGCGCGGCTTGAGATAGTCAAGCGCG
ACTGAGCGAGATAGCGAAGGAGACGCGAGGGTTTGGAGCGGATCTCAGGCAAGGTTGAAGAGCGGTCAGAAATTGTCAAGGAAAGTCAACGAAAGCTGAGCAA
GTACGAGGTTCCGCGGAGAGAGCTGTTATCCACGAGCAGATAACGCGGAGCTCAAGGACTACAGGCCACCGGCCGACGTAAGCCATAGCGAAAGCTTTGGCCGCGAGAGT
GTTAAATCCGCGCGGAACGTGATAAGCTACATCGTTCTGAAGGCTCCGGAAGATAGCGACAGGCGGATTCCTTCGACGAGTTCGACCCGACGAAAGCACAAGTACGATG
CGGACTACTACATCGAGAACCAAGTTCTGCCGCGAGTTGAGAGAATCTCAGGGCTTGGCTACCGCAAGGAAGACCTGCGCTACCAAGAAGACGAGGCGAGTGGCGG
GTGGCTGAAGCCGAAGGGAAGAAGAAG//

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TAG

Sso7d - JDF-3 fusion protein (Fig. 17-RRR)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG //

Fig. 17 RRR (cont)

ATGATCCTTGACGTTGATTACATCACCGAATGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCAGTTCAAGATTGAATACGACCGCAGTTGAGCCCTACTTCT
ACGGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGAGAGGCCACGGCAGGGTCGTTAAGGTTAAGCCGCCGGAAGAGTGAAAGAAAAATTCCCTGG
CAGTCTGTGAGGTCTGGTCTCTACTTACCGCACCCCGCAGGACXXXCCGCCAATCCCGCACAAATAAGGAAGCACCCCGCGGTCACTCGACATCTACGAGTACGACATACCC
TTGCCAAGCGCTACCTCATAGACAAAGGCCCTAATCCCGATGGAAGGTGAGGAAGCTTAACCTCATGTCTTGAATGAGAGCGCTCTACCAAGGAGGAGAAAGATTGGAA
CCGGCCGATTTCTGATGATAAGCTACGCCGATGAAAGCGAGCGCGCGTGATAACCTGGAAGAAGATCGACCTTCTTACGTTGAGGTTGTCTCCACCGAAGAGAGATGATTAA
GCGCTTCTGAGGTCGTTAAGGAGAAGACCCGGACGTGCTGATAACATCAACGGCGACAACTTCGACTTCGCCCTACCTGAATAAGCGCTGTGAGAACTTGGCGTGAGCTTT
ACCCTCGGAGGAGCGGAGCGAGCCGAAGATAAGCGCATGGGGACAGGTTTGGGTGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCATAGCGGCACCATAA
ACCTCCCGACCTACACCCCTTGAGGCTGTATACGAGCGGTTTTCGGCAAGCCCAAGGAAGAGTTACGCCGAGAGATAGCCACCGCTGGGAGACCGGCGAGGGGCTTGAGAG
GGTCGCGCGCTACTCGATGAGGACCGGAGGGTTACCTACGAGCTTGGCAGGAGTTCTCCCGATGAGGCCCAAGCTTCCAGGCTCATCGGCCAAGGCTCTGGGACGTTTC
CGCTCCAGCACCGGCAACCTCGTGAGTGTCTCTTAAGGAAGGCTTACGAGAGGAACGAACCTGCTCCACAAGCCCGCAGAGAGGAGCTGGCGAGGAGAAAGGGGGCT
ACGCCGGTGGCTACGTCAAGGAGCCGGAGCGGGGACTGTGGGACAAATATCGTGTATCTAGACTTTCGTAGTCTTACCTTCAATCATATCACCCACAACGTTCTGCCAGATAC
GCTCAACCGCGAGGGGTAGGAGCTACGACGTTGCCCGCAGGTCGCTCAAGTCTGCAAGGACTTCCCGGCTTCATTCGAGCCCTGCTCGGAACCTGTGAGGAAAGG
CAGAAGATAAAGAGGAAGATGAAGGCAACTCTGACCCGCTGGAAGAAGATCTCTCGATTACAGGCAACGCGGCTATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT
ATGCCAGGGCAAGATGGTACT⁴TCAGGGAGTCCGCCGAGAGCGTTACGGCATGGGGAAGGAGTACATCGAAATGGTTCATCAGAGAGCTTGAGGAAAGTTGCGTTTAAAGTCTC
CTATGCAGACACAGACGGTCTCCATGCCACCATTTCTGGAGCGGACGCTGAACAGTCAAGAAAAAGGCAATGGAGTTCTTAACTATATCAATCCCAACTGCCCGCTTCTC
GAACTCGAATACGAGGCTTCTACGTGAGGGCTTCTTCTGTCACGAAGAAAAAGTACGCGGTCAATCGAGGAGGGCAAGATAACCAACGCGGGCTTGAGATAGTCAAGCGCG
ACTGGAGCGAGATAGCGAAGGAGACCGCAGCGGAGGGTTTGGAGCGGATACTCAGGCAAGGTGACGTTGAAGAGGCCGTGAGAAATGTCAAGGAAAGTCAACGAAAGCTGAGCAA
GTACGAGGTTCCGCCGAGAAAGCTGTTATCCACGAGCAGATAACGCCGAGCTCAAGGACTACAAGGCCACCGGCCGACGTAGCCATAGCGAAAGCGTTTGGCCGCCAGAGGT
GTTAAATCCGGCCCGGAATGTGATAAGCTACATCGTTCTGAAGGCTCCGGAAGGATAGCGACAGGCGGATTCCTTGAAGGTTGACCCGACGAAGCAACAGTACGATG
CGACTACTACATCGAGAACCAAGTTCTGCCCGCAGTTGAGAGAATCCTCAGGGCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAAGAAGACGAGGCAAGTTCGGGCTTGGCGC
GTGGCTGAAGCCGAAGGGAAGAAGAGTGA

Fig. 19

Synthetic Sso7d gene

GCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAAGAGGTTAGACATCTCCAA
5 GATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTACGACGAGGG
CGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAGGACGCGCCGAAGGAGC
TGCTGCAGATGCTGGAGAAG
CAGAAAAAG

The amino acid sequence of Sso7d.

ATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDAPKELLQ
MLEKQKK

The DNA sequence encoding the Sso7d- Δ Taq fusion protein

15 ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA
GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC
TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAG
GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGGCGG
TGTCACTAGTCCCAAGGCCTGGAGGAGGCCCCCTGGCCCCCGCCGGAAGGGGGCC
20 TTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCT
GGCCGCCGCCAGGGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCT
CAGGGACCTGAAGGAGGCGCGGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGC
CCTGAGGGAAGGCCTTGGCCTCCCGCCCCGGCGACGACCCCATGCTCCTCGCCTAC
CTCCTGGACCCTTCCAACACCACCCCCGAGGGGGTGGCCCCGGCGCTACGGCGGG
25 GAGTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTTCCGAGAGGCTCTTCGCC
AACCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAG
GTGGAGAGGCCCCCTTTCCGCTGTCCTGGCCCCACATGGAGGCCACGGGGGTGCGC
CTGGACGTGGCCTATCTCAGGGCCTTGTCCTTGGAGGTGGCCGAGGAGATCGCCC
GCCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCG
30 GGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAA
GACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCCGTCCTGGAGGCCCTCCG
CGAGGCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAGCT
GAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCAGGACGGGCCG
CCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTC

Fig. 19 (cont)

CGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGC
CGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAG
ATAGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCT
TCCAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGGATGTTTCGGCGTCC
5 CCCGGGAGGCCGTGGACCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCG
GGGTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGCTAGCCATCCCTTA
CGAGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGG
GCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGGTACGTGGAGAC
CCTCTTCGGCCGCCGCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGT
10 GCGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGC
CGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGG
GGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCCAAAAGA
GAGGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGGAGGGGGGTGTATCC
CCTGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGC
15 CAAGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATCATCATCATTAA
A

The amino acid sequence of Sso7d- Δ Taq fusion protein

MITNSSATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDA
20 PKELLQMLEKQKKGGGVTS PKALEEAPWPPPEGAFVGFVLSRKEPMWADLLALAA
ARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLLDP
SNTTPEGVARRYGGEWTEEAGERAAALSERLFANLWGRLEGEERLLWLYREVERPLS
AVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERVLF
DELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPLIH
25 PRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFIAEEGWLLVALDYS
QIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFGV
LYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETLFGRR
RYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKCLAMVKLFPRLEEMGARMMLL
QVHDELVLEAPKERAEEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKEGIDGR
30 GGGGHHHHHHH

The DNA sequence encoding the Sso7d-Taq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA

163/186

Fig. 19 (cont)

GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC
 TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAG
 GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG
 TGTCAC TAGTGGGATGCTGCCCCCTCTTTGAGCCCAAGGGCCGGGTCTCCTGGTG
 5 GACGGCCACCACCTGGCCTACCGCACCTTCCACGCCCTGAAGGGCCTCACCACCA
 GCCGGGGGGAGCCGGTGCAGGCGGTCTACGGCTTCGCCAAGAGCCTCCTCAAGG
 CCCTCAAGGAGGACGGGGACGCGGTGATCGTGGTCTTTGACGCCAAGGCCCCCT
 CCTTCCGCCACGAGGCCTACGGGGGGGTACAAGGCGGGCCGGGGCCCCCACGCCAG
 AGGACTTTCCCCGGCAACTCGCCCTCATCAAGGAGCTGGTGGACCTCCTGGGGCT
 10 GGCGCGCCTCGAGGTCCCGGGCTACGAGGCGGACGACGTCCTGGCCAGCCTGGC
 CAAGAAGGCGGAAAAGGAGGGCTACGAGGTCCGCATCCTCACCGCCGACAAAG
 ACCTTTACCAGCTCCTTTCCGACCGCATCCACGTCCTCCACCCCGAGGGGTACCT
 CATCACCCCGGCCTGGCTTTGGGAAAAGTACGGCCTGAGGCCCGACCAAGTGGGC
 CGACTACCGGGCCCTGACCGGGGACGAGTCCGACAACCTTCCCGGGGTCAAGGG
 15 CATCGGGGAGAAGACGGCGAGGAAGCTTCTGGAGGAGTGGGGGAGCCTGGAAG
 CCCTCCTCAAGAACCTGGACCGGCTGAAGCCCGCCATCCGGGAGAAGATCCTGG
 CCCACATGGACGATCTGAAGCTCTCCTGGGACCTGGCCAAGGTGCGCACCGACCT
 GCCCCTGGAGGTGGACTTCGCCAAAAGGCGGGAGCCCGACCGGGAGAGGCTTAG
 GGCCTTTCTGGAGAGGCTTGAGTTTGGCAGCCTCCTCCACGAGTTCGGCCTTCTG
 20 GAAAGCCCCAAGGCCTGGAGGAGGCCCCCTGGCCCCCGCCGGAAGGGGCCTTC
 GTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCTGG
 CCGCCGCCAGGGGGGGGCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCTCA
 GGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGCCC
 TGAGGGAAGGCCTTGGCCTCCCGCCCCGGCGACGACCCCATGCTCCTCGCCTACCT
 25 CCTGGACCCTTCCAACACCACCCCGAGGGGGTGGCCCGGCGCTACGGCGGGGA
 GTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTTCCGAGAGGCTCTTCGCCAA
 CCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAGGT
 GGAGAGGCCCCCTTTCCGCTGTCCTGGCCCACATGGAGGCCACGGGGGTGCGCCT
 GGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGCCGAGGAGATCGCCCG
 30 CCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGG
 GACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAAG
 ACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCGCTCCTGGAGGCCCTCCGC
 GAGGCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAGCTG
 AAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCAGGACGGGGCCGCC

Fig. 19 (cont)

TCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTCCG
ATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGCCG
GGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAGAT
AGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCTTC
5 CAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGGATGTTTCGGCGTCCCC
CGGGAGGCCGTGGACCCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCGGG
GTCCTCTACGGCATGTGCGGCCACCGCCTCTCCCAGGAGCTAGCCATCCCTTACG
AGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGGGC
CTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTGGAGACCC
10 TCTTCGGCCGCGCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGTGC
GGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCCGTCCAGGGCACCGCCGCCG
ACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGGGG
CCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCCAAAAGAGA
GGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGGAGGGGGTGTATCCCC
15 TGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGCCA
AGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATCATCATCATTA

The amino acid sequence of Sso7d-Taq fusion protein.

MITNSSATVKFKYKGEEKEVDISKIKKVWRVVGKMISFTYDEGGGKTGRGAVSEKDA
20 PKELLQMLEKQKKGGGVTSFMLPLFEPKGRVLLVDGHHLAYRTFHALKGLTTSRGE
PVQAVYGFASLLKALKEDGDAVIVVFDKAPSFRHEAYGGYKAGRPTPEDFPRQ
LALIKELVDLLGLARLEVPGYEADDVLASLAKKAEKEGYEVRILTADKDLYQLLSDR
IHVLHPEGYLITPAWLWEKYGLRPDQWADYRALTGDESDNLPGVKGIGEKTARKLL
EEWGSLEALLKNLDRLKPAIREKILAHMDDLKLSWDLAKVRTDLPLEVDFAKRREP
25 DRERLRAFLERLEFGSLLHEFGLLESPKALEEAPWPPPEGAFVGVLSRKEPMWADL
LALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLA
YLLDPSNTTPEGVARRYGGEWTEEAGERAAALSERLFANLWGRLEGEERLLWLYREV
ERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQL
ERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPL
30 PDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIIRAFIAEEGWLLVA
LDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTI
NFGVLYGMSAHRLSQELAIPEYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETL
FGRRRYVPDLEARVKS VREAAERMAFNMPVQGTAA DLMK LAMVKLFPRLEEMGA

Fig. 19 (cont)

RMLLQVHDEL VLEAPKERA EAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKE
GIDGRGGGGHHHHHH

The DNA sequence encoding the Pfu-Sso7d fusion protein

5 ATGATTTTAGATGTGGATTACATAACTGAAGAAGGAAAACCTGTTATTAGGCTAT
TCAAAAAAGAGAACGGAAAATTTAAGATAGAGCATGATAGAACTTTTAGACCAT
ACATTTACGCTCTTCTCAGGGATGATTCAAAGATTGAAGAAGTTAAGAAAATAAC
GGGGGAAAGGCATGGAAAGATTGTGAGAATTGTTGATGTAGAGAAGGTTGAGAA
AAAGTTTCTCGGCAAGCCTATTACCGTGTGGAACTTTATTTGGAACATCCCCAA
10 GATGTTCCCACTATTAGAGAAAAAGTTAGAGAACATCCAGCAGTTGTGGACATCT
TCGAATACGATATTCCATTTGCAAAGAGATACCTCATCGACAAAGGCCTAATACC
AATGGAGGGGGGAAGAAGAGCTAAAGATTCTTGCCTTCGATATAGAAACCCTCTA
TCACGAAGGAGAAGAGTTTGGAAAAGGCCCAATTATAATGATTAGTTATGCAGA
TGAAAATGAAGCAAAGGTGATTACTTGGAAAAACATAGATCTTCCATACGTTGA
15 GGTGTATCAAGCGAGAGAGAGATGATAAAGAGATTTCTCAGGATTATCAGGGA
GAAGGATCCTGACATTATAGTTACTTATAATGGAGACTCATTGACTTCCCATAT
TTAGCGAAAAGGGCAGAAAACTTGGGATTAAATTAACCATTGGAAGAGATGGA
AGCGAGCCCAAGATGCAGAGAATAGGCGATATGACGGCTGTAGAAGTCAAGGG
AAGAATACATTTGACTTGTATCATGTAATAACAAGGACAATAAATCTCCAACA
20 TACACACTAGAGGCTGTATATGAAGCAATTTTGGAAAGCCAAAGGAGAAGGTA
TACGCCGACGAGATAGCAAAAGCCTGGGAAAGTGGAGAGAACCTTGAGAGAGTT
GCCAAATACTCGATGGAAGATGCAAAGGCAACTTATGAACTCGGGAAAGAATTC
CTTCCAATGGAAATTCAGCTTTCAAGATTAGTTGGACAACCTTTATGGGATGTTT
CAAGGTCAAGCACAGGGAACCTTGTAGAGTGGTTCTTACTTAGGAAAGCCTACG
25 AAAGAAACGAAGTAGCTCCAAACAAGCCAAGTGAAGAGGAGTATCAAAGAAGG
CTCAGGGAGAGCTACACAGGTGGATTCGTTAAAGAGCCAGAAAAGGGGTTGTGG
GAAAACATAGTATACCTAGATTTTAGAGCCCTATATCCCTCGATTATAATTACCC
ACAATGTTTCTCCCGATACTCTAAATCTTGAGGGGATGCAAGAACTATGATATCGC
TCCTCAAGTAGGCCACAAGTTCTGCAAGGACATCCCTGGTTTTATACCAAGTCTC
30 TTGGGACATTTGTTAGAGGAAAGACAAAAGATTAAGACAAAAATGAAGGAAACT
CAAGATCCTATAGAAAAAATACTCCTTGACTATAGACAAAAAGCGATAAACTC
TTAGCAAATTCTTTCTACGGATATTATGGCTATGCAAAGCAAGATGGTACTGTA
AGGAGTGTGCTGAGAGCGTTACTGCCTGGGGAAGAAAGTACATCGAGTTAGTAT
GGAAGGAGCTCGAAGAAAAGTTTGGATTAAAGTCCTCTACATTGACACTGATG

166/186

Fig. 19 (cont)

GTCTCTATGCAACTATCCCAGGAGGAGAAAGTGAGGAAATAAAGAAAAAGGCTC
TAGAATTTGTAAAATACATAAATTCAAAGCTCCCTGGACTGCTAGAGCTTGAATA
TGAAGGGTTTTATAAGAGGGGGATTCTTCGTTACGAAGAAGAGGTATGCAGTAAT
AGATGAAGAAGGAAAAGTCATTACTCGTGGTTTAGAGATAGTTAGGAGAGATTG
5 GAGTGAAATTGCAAAAGAAACTCAAGCTAGAGTTTTGGAGACAATACTAAAACA
CGGAGATGTTGAAGAAGCTGTGAGAATAGTAAAAGAAGTAATACAAAAGCTTGC
CAATTATGAAATTCCACCAGAGAAGCTCGCAATATATGAGCAGATAACAAGACC
ATTACATGAGTATAAGGCGATAGGTCCTCACGTAGCTGTTGCAAAGAACTAGCT
GCTAAAGGAGTTAAAATAAAGCCAGGAATGGTAATTGGATACATAGTACTTAGA
10 GGCGATGGTCCAATTAGCAATAGGGCAATTCTAGCTGAGGAATACGATCCCAAA
AAGCACAAGTATGACGCAGAATATTACATTGAGAACCAGGTTCTTCCAGCGGTA
CTTAGGATATTGGAGGGATTGGATACAGAAAGGAAGACCTCAGATACCAAAAAG
ACAAGACAAGTCGGCCTAACTTCCTGGCTTAACATTAAAAAATCCGGTACCGGC
GGTGGCGGTGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAAGAGGTAGA
15 CATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTAC
GACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAGGACGCGCC
GAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGTGA

The amino acid sequence of the Pfu-Sso7d fusion protein

20 MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYTYALLRDDSKIEEVKKITGERH
GKIVRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKVVREHPAVVDIFEYDIPFA
KRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKGPIIMISYADENEAKVITWKNID
LPYVEVVSSSEREMIKRFLRIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGS
EPKMQRIGDMTAVEVKGRIFDLHYVITRTINLPTYTLEAVYEAFGKPKKEKVYADEI
25 AKAWESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSSTGN
LVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESYTGGFVKEPEKGLWENIVYLDLR
ALYPSIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQKIKTK
MKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIE
LVWKELEEKFGFKVLYIDTDGLYATIPGGESEEEKKALEFVKYNSKLPGLLELEYE
30 GFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDWSEIAKETQARVLETILKHGDVEE
AVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVKIKPG
MVGIVYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVLRILEGFGYRKED
LRYQKTRQVGLTSWLNKKSGTGGGGATVKFKYKGEEKEVDISKIKKVWRVVGKMIS
FTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKK

167/186

Fig 19 (cont)

The DNA sequence encoding the Sac7d-ΔTaq fusion protein

ATGATTACGAATTCGACGGTGAAGGTAAAGTTCAAGTATAAGGGTGAAGAGAAA
GAAGTAGACACTTCAAAGATAAAGAAGGTTTGGAGAGTAGGCAAAATGGTGTCC
5 TTTACCTATGACGACAATGGTAAGACAGGTAGAGGAGCTGTAAGCGAGAAAGAT
GCTCCAAAAGAATTATTAGACATGTTAGCAAGAGCAGAAAGAGAGAAGAAAGG
CGGCGGTGTCACTAGTCCCAAGGCCCTGGAGGAGGCCCCCTGGCCCCCGCCGGA
AGGGGCCTTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTT
CTGGCCCTGGCCGCCGCCAGGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTAT
10 AAAGCCCTCAGGGACCTGAAGGAGGCGCGGGGGGCTTCTCGCCAAAGACCTGAGC
GTTCTGGCCCTGAGGGAAGGCCTTGGCCTCCCGCCCCGGCGACGACCCCATGCTCC
TCGCCTACCTCCTGGACCCTTCCAACACCACCCCCGAGGGGGTGGCCCCGGCGCTA
CGGCGGGGAGTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTTCCGAGAGGC
TCTTCGCCAACCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTA
15 CCGGGAGGTGGAGAGGCCCTTTCCGCTGTCCTGGCCCACATGGAGGCCACGGG
GGTGCGCCTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGCCGAGGA
GATCGCCCGCCTCGAGGCCGGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCA
ACTCCCGGGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTCCCGCCAT
CGGCAAGACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCGTCCTGGAGGC
20 CCTCCGCGAGGCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCAC
CAAGCTGAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCAGGACG
GGCCGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGT
AGCTCCGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGGCAGAGGA
TCCGCCGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAG
25 CCAGATAGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAACCTGATCCG
GGTCTTCCAGGAGGGGGCGGGACATCCACACGGAGACCGCCAGCTGGATGTTTCGG
CGTCCCCCGGGAGGCCGTGGACCCCTGATGCGCCGGGGCGGCCAAGACCATCAA
CTTCGGGGTCCTCTACGGCATGTGCGGCCACCGCCTCTCCCAGGAGCTAGCCATC
CCTTACGAGGAGGCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGG
30 TGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTG
GAGACCCTCTTCGGCCGCGCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAG
AGCGTGCGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCCGTCCAGGGCACC
GCCGCCGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAA

Fig. 19 (cont)

ATGGGGGGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGGCCCCA
AAAGAGAGGGCGGAGGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGGAGGGGGT
GTATCCCCTGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCT
CTCCGCCAAGGAGGGCATTGATGGCCGCGGCGGAGGCGGGGCATCATCATCA
5 TCATTAA

The amino acid sequence of the Sac7d-ΔTaq fusion protein

MITNSTVKVKFKYKGEEKEVDTSKIKKVWRVGKMOVSTYDDNGKTGRGAVSEKDA
PKELLDMLARAEREKKGGGVTSKALEEAPWPPPEGAFVGFVLSRKEPMWADLLAL
10 AAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLL
DPSNTTPEGVARRYGGEWTEEAGERAAALSERLFANLWGRLEGEERLLWLYREVERP
LSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERV
LFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPLDI
HPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFIAEEGWLLVALDY
15 SQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFG
VLYGMSAHRLSQELAIPEYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETLFGR
RRYVPDLEARVKSVREAAERMAFNMPVQGTAAADLMKLMVKLFPRLEEMGARMML
LQVHDELVLEAPKERAEEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKEGIDG
RGGGGHHHHHHH

20

The DNA sequence encoding the PL-ΔTaq fusion protein

ATGATTACGAATTCGAAGAAAAAGAAAAAGAAAAAGCGTAAGAAACGCAAAAA
GAAAAAGAAAGGCGGCGGTGTCACTAGTGGCGCAACCGTAAAGTTCAAGTACAA
AGGCGAAGAAAAAGAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGG
25 GCAAGATGATCTCCTTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTG
CGGTAAGCGAAAAGGACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAG
AAAAAGGGCGGCGGTGTCAACAGTCCCAAGGCCCTGGAGGAGGCCCCCTGGCCC
CCGCCGGAAGGGGGCCTTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGG
CCGATCTTCTGGCCCTGGCCGCCGCGCAGGGGGGGGCGGGTCCACCGGGGCCCCCG
30 AGCCTTATAAAGCCCTCAGGGACCTGAAGGAGGCGCGGGGGGCTTCTCGCCAAAG
ACCTGAGCGTTCTGGCCCTGAGGGAAGGCCTTGGCCTCCCGCCCCGGCGACGACCC
CATGCTCCTCGCCTACCTCCTGGACCCTTCCAACACCACCCCCGAGGGGGGTGGCC
CGGCGCTACGGCGGGGAGTGGACGGAGGAGGCGGGGGGAGCGGGGCCGCCCTTTCC

169/186

Fig. 19 (cont)

GAGAGGCTCTTCGCCAACCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTT
TGGCTTTACCGGGAGGTGGAGAGGCCCCCTTTCCGCTGTCCTGGCCCACATGGAGG
CCACGGGGGTGCGCCTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGC
CGAGGAGATCGCCCGCCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTC
5 AACCTCAACTCCCGGGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTC
CCGCCATCGGCAAGACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCCGTCC
TGGAGGCCCTCCGCGAGGCCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGG
AGCTCACCAAGCTGAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCC
CAGGACGGGGCCGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAG
10 GCTAAGTAGCTCCGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGG
CAGAGGATCCGCCGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTG
GACTATAGCCAGATAGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAAC
CTGATCCGGGTCTTCCAGGAGGGGGCGGGACATCCACACGGAGACCGCCAGCTGG
ATGTTTCGGCGTCCCCCGGGAGGCCGTGGACCCCCTGATGCGCCGGGCGGCCAAG
15 ACCATCAACTTCGGGGTCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGC
TAGCCATCCCTTACGAGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTT
CCCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGG
GGTACGTGGAGACCCTCTTCGGCCGCCGCGCTACGTGCCAGACCTAGAGGCC
GGGTGAAGAGCGTGCGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCCGTCC
20 AGGGCACCGCCGCCGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCT
GGAGGAAATGGGGGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGA
GGCCCCAAAAGAGAGGGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGG
AGGGGGTGTATCCCCTGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGG
ACTGGCTCTCCGCCAAGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATC
25 ATCATCATCATTAA

The amino acid sequence of PL-ΔTaq fusion protein

MITNSKKKKKKRKKRKKKKKGGGVTS GATVKFKYKGEEKEVDISKIKKVWRVGK
MISFTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKKGGGVTS PKALEEAPWPPPEG
30 AFVGFVLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVL
ALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAALSERLFAN
LWGRLEGEERLLWLYREVERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLE
AEVFRLAGHPFNLNSRDQLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIV

Fig. 19 (cont)

EKILQYRELTKLKSTYIDPLPDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTP
LGQRIRRAFIAEEGWLLVALDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMF
GVPREAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVR
AWIEKTLEEGRRRGYVETLFGRRRYVPDLEARVKSVREAAERMAFNMPVQGTAAAD
5 LMKLAMVKLFPRL EEMGARMLLQVHDEL VLEAPKERA EAVARLAKEVM EGVYPL
AVPLEVEVGIGEDWLSAKEGIDGRGGGGGHHHHHH

PRIMER L71F

5'-CCTGCTCTGCCGCTTCACGC-3'

10

PRIMER L71R

5'-GCACAGCGGCTGGCTGAGGA-3'

PRIMER L18015F

15 5'-TGACGGAGGATAACGCCAGCAG-3'

PRIMER L23474R

5'-GAAAGACGA TGGGTCGCTAATACGC-3'

20

PRIMER L18015F

5'-TGACGGAGGATAAC GCCAGCAG-3'

PRIMER L29930R

5'-GGGGTTGGAGGTCAATGGGTTC-3'

25

PRIMER L30350F

5'-CCTGCTCTGCCGCTTCACGC-3'

PRIMER L35121R

30 5'-CACATGGTACAGCAAGCCTGGC-3'

PRIMER L2089F

5'-CCCGTATCTGCTGGGA TACTGGC-3

17/1/86

Fig. 19 (cont.)

PRIMER L7112R

5'-CAGCGGTGCTGACTGAATCATGG-3'

PRIMER L30350F

5 5'-CCTGCCTGCCGCTTCACGC-3'

PRIMER L40547R

5'-CCAATACCCGTTTCA TCGCGGC-3'

10 **PRIMER H-Amelo-Y**

5'-CCACCTCATCCTGG GCACC-3'

PRIMER H-Amelo-YR

5'-GCTTGAGGCCAACCATCAGAGC-3'

15

Human beta-globin primer 536F

5'-GGTTGGCCAATCTACTCCCAGG-3'

Human beta-globin primer 536R

20 5'-GCTCACTCAGTGTGGCAAAG-3'

Human beta-globin primer 1408R

5'-GATTAGCAAAAGGGCCTAGCTTGG-3'

25

172/186

PURIFIED THERMOSTABLE PYROCOCCLUS FURIOSUS DNA POLYMERASE I

AMINO ACID SEQUENCE (SEQ ID NO: 62)

Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
20 25 30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Ser Lys Ile
35 40 45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
50 55 60

FIG. 20A

173/186

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65 70 75 80

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
85 90 95

Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125

Met Glu Gly Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145 150 155 160

174/186

Fig. 20B

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
180 185 190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
195 200 205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
210 215 220

Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225 230 235 240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
245 250 255

175/186

Fig. 20C

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
260 265 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
275 280 285

Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
290 295 300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305 310 315 320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
325 330 335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350

176/186

FIG. 20D

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
355 360 365

Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser
370 375 380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385 390 395 400

Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Thr
405 410 415

His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr
420 425 430

Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
435 440 445

Fig. 20E

177/186

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Arg Gln Lys Ile
450 455 460

Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu
465 470 475 480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
485 490 495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
500 505 510

Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu
515 520 525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
530 535 540

178/186

FIG. 20F

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys
545 550 555 560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
565 570 575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Val Thr Lys
580 585 590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly
595 600 605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
610 615 620

Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala
625 630 635 640

179/186

FIG. 206

Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile
645 650 655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
660 665 670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
675 680 685

Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
690 695 700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705 710 715 720

Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
725 730 735

180/186

FIG. 20H

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
740 745 750

Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser
755 760 765

Trp Leu Asn Ile Lys Lys Ser
770 775

PURIFIED THERMOSTABLE PYROCOCCLUS FURIOSUS DNA POLYMERASE I

NUCLEOTIDE SEQUENCE (SEQ ID NO: 61)

ccctggtcct ggggccacat atatgttctt actcgccctt atgaagaatc cccagtcgc 60

tctaacctgg gttatagtga caaatcttcc tcaccaccg cccaagaagg ttatttctat 120

Fig. 20I

981/181

caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag 180
 gttttatact ccaaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga 240
 ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaataatt 300
 taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc 360
 aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt 420
 tgatgtagag aaggttgaga aaaagtcttct cggcaagcct attaccgtgt ggaaacttta 480
 tttggaacat cccaagatg ttcccactat tagagaaaaa gtagagaac atccagcagt 540
 tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaaggcct 600
 aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta 660
 tcacgaagga gaagagttag gaaaaggccc aattataatg attagttatg cagatgaaaa 720
 tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag 780

182/186

FIG. 20J

cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat 840
 agttacttat aatggagact cattcgactt ccatattta gcgaaaaggg cagaaaaact 900
 tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga 960
 tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag 1020
 gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttggaagcc 1080
 aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga 1140
 gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt 1200
 cctccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag 1260
 gtcaagcaca gggaacccttg tagagtggtt ctacttagg aaagcctacg aaagaaacga 1320
 agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac 1380
 aggtggattc gttaaagagc cagaaaaggg gtgtgtggaa aacatagtat acctagattt 1440
 tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaattct 1500

183/186

FIG. 20K

tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat 1560
 ccctgggttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac 1620
 aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc 1680
 gataaaactc ttagcaaat ctttctacgg atattatggc tatgcaaaag caagatggta 1740
 ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg 1800
 gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggctctcta 1860
 tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aattgtgtaa 1920
 atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag 1980
 gggattcttc gttacgaaga agaggatgc agtaatagat gaagaaggaa aagtcattac 2040
 tcgtgggtta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag 2100
 agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga 2160

84/86

FIG. 20L

agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca 2220
 gataacaaga ccattacatg agtataaggc gataggctct cacgtagctg ttgcaaagaa 2280
 actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag 2340
 aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca 2400
 caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtag ttaggatatt 2460
 ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct 2520
 aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt 2580
 tctaaccctt ttctatgaa gaagaactga gcaggaatta ccagttcttc cgttatttta 2640
 tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc 2700
 ttgctaagt gaatagaata aacaacatca ctcaattcaa acgccttcgt tagaaatggt 2760
 ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct 2820
 cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct 2880

185/106

FIG. 20M

tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt 2940
tttgctccaa gcagagccgc tccaatggat aacacccctg ttccgcacc caagtccgct 3000
acaattttt ccttgatat cctaattgtat aagcaagcca aaggagagta gatgctacct 3060
ttccgggagt tttgtattgc tctagccaag gttgggatt tttgaatcct ttaactctgg 3120
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt 3180
taacttttac agaaataact gtctcaaatt atgacaaactc ttgacatttt tacttcatta 3240
ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnn nngtcctctc 3300
ctcgatttcc ttggttggtgc tccatatgat aagcttccaa agtgggtgtt cagactttta 3360
gacactcaa taccagacga caatggtgtg ctcaactcaag ccccatatgg gttgagaaaa 3420
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgtgtagc tcntcccnga 3480
aagattgaga tgttcttgg 3499

186/186

FIG. 20N